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GenCore version 5.1.6
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March 10, 2005, 10:55:58; Search time 66.0263 Seconds (without alignments) 76.150 Million cell updates/sec Run on:

US-09-766-412-30 66 1 QPVLHLVALNTPL 13 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 Total number of hits satisfying chosen parameters:

2105692 segs, 386760381 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

geneseqp1980s:* geneseqp2000s:* geneseqp2001s:* geneseqp2001s:* geneseqp2003s:* geneseqp2003bs:* geneseqp2003bs:* A_Geneseq_16Dec04:*
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2: geneseqp1990s:*
3: geneseqp2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aab74256 Exemplary	Aab80862 Angiostat	Abg97539 Antiangio	G	Aay94321 Mouse end	1 Endost	Ada43206 Mouse end	Adm99393 Human end	Aab49806 Murine en	Aab35584 Antiangio	Aab71931 Murine si	Aam49504 Mouse end	Aay18409 Endostati	Aay08689 Murine en	Aay70258 Murine an	Aab49380 Murine en	Abg31793 Human end	Abu64290 Murine en	Aay06197 Anti-angi	Aab28398 Murine en	Aau77950 Amino aci	Aae02031 Murine en	Aab71930 Murine en	Abb79902 Mouse end	Adn00602 Murine en
SUMMAKIES	ID	AAB74256	AAB80862	ABG97539	AAW16596	AAY94321	AAM48821	ADA43206	ADM99393	AAB49806	AAB35584	AAB71931	AAM49504	AAY18409	AAY08689	AAY70258	AAB49380	ABG31793	ABU64290	AAY06197	AAB28398	AAU77950	AAE02031	AAB71930	ABB79902	ADN00602
	Length DB	13 4	13 4	13 5			20 5	20 7	20 8	23 4	39 4	42 4	183 5		184 2		184 4	184 5	184 7		191 3		Ī	207 4	207 5	207 8
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Amino Murine Murine	Mouse Mouse Mouse	Abo84584 Mouse can Aab49850 Human end Adk40308 Collagen Aab49866 Human end	Abg31791 Human end Abg31787 Human end Aay94324 Alternate Aau00900 Human End	Human Human Human	Human Human
ADO43904 AAY08691 AAY08692	AAY25114 AAW26328 AAW92297 ABO84585	AEC84584 AAB49850 ADK40308 AAB49866	ABG31791 ABG31787 AAY94324 AAU00900	AAU00901 AAU00899 AAU00898	AAY59622 AAY94323
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ALIGNMENTS

374 374	म 1 256
e X	AAB74256 standard; peptide; 13 AA.
	AAB74256;
1	23-MAY-2001 (first entry)
智	Exemplary anti-angiogenic peptide #30.
122	Anti-angiogenesis; plasminogen; ${\tt VEGF}$; vascular endothelial growth factor; ${\tt FLT-1}$; tumour; metastasis; cancer.
¥8	Homo sapiens.
	WO200118030-A2.
X A B	15-MAR-2001,
X ii.	01-SEP-2000; 2000WO-SG000131.
X X	03-SEP-1999; 99SG-00004310.
3	(UYSI-) UNIV SINGAPORE NAT.
žE;	Ge R, Kini RM;
2 K S	WPI; 2001-257785/26.
	Peptides comprising a portion of a protein selected from plasminogen,
	endostatin, VEGF, FLT-1 and KDK/FLK-1 are useru1 for treating primary

rrom plasminogen, treating primary 101 nserni are endostatin, VEGF, FLT-1 and KDR/FLK-1 tumor growth.

Claim 7; Page 18; 34pp; English.

The present invention relates to anti-angiogenesis peptides from a portion of a selected from plasminogen, endostatin, VEGF or FLT-1. The invention is used to prevent or treat primary tumour growth or metastasis or undesired angiogenesis

Sequence 13 AA;

ö Gaps ö Query Match 100.0%; Score 66, DB 4; Length 13; Best Local Similarity 100.0%; Pred. No. 3.5e-05; Matches 13; Conservative 0; Mismatches 0; Indels

1 QPVEHEVAENTPE 13

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The invention discloses a peptide comprising a portion of a protein e.g. plasminogen, endostatin (Endo-1-4), vascular endothelial growth factor (VEGE), FIL-1 or kinase insert domain containing receptor/FLK-1. These peptides are able to act as potent angiogenic inhibitors (Angio-1-5) inhibiting endothelial cell proliferation and retarding tumour growth. Angiogenesis is the process of new blood vessel formation from precessing the structures. It plays an important on in migration and assembly into tubule structures. It plays an important role in normal physiological functions such as embryonic development and wound healing. Inappropriate angiogenesis is also associated with various pathological conditions including tumour growth and metastasis, rheumatoid arthritis and psoriasis. Anticancer therapy by inhibiting tumour angiogenesis is called antiangiogenic therapy and pharmacological and pharmacological and pharmacological such these interactions. The peptides are useful for preventing or treating undesired angiogenesis and primary tumour growth or metastasis. The sequences presented in ABG97510-ABG97559 are examples of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Endostatin; angiogenesis; cancer; tumour; rheumatoid arthritis; psoriasis; ocular; Osler-Webber Syndrome; myocardial; telangiectasia; plaque neovascularisation; haemophiliac joint; angiofibroma; inhibitor; wound granulation; intestinal adhesion; atherosclerosis; scleroderma; hypertrophic scar; cat scratch disease; Rochele minalia quintosa; Helicobacter pylori ulcer; birth control; collagen alpha type XVIII.
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel peptide for preventing/treating undesired angiogenesis, has a portion of a protein e.g. plasminogen, endostatin, and potent antiangiogenic activity and endothelial cell proliferation inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 66; DB 5; Length 13; 100.0%; Pred. No. 3.5e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW16596 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 9; Page 10; 24pp; English.
                                                                                                                        22-JAN-2001; 2001US-00766412
                                                                                                                                                                         98US-0099313P
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                                                                                                                          (KINI/) KINI R M.
                          US2002103129-A1
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                                                                                                                                                                         04-SEP-1998;
30-AUG-1999;
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                                                                      01-AUG-2002
                                                                                                                                                                                                                                                (GERR/) GE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        activity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            undestrable angiogenesis. Angiogenesis is the process of new blood vessel formation from pre-existing vessels. Inappropriate angiogenesis is associated with various pathological conditions including solid tumour growth and metastasis. The present peptide can be used to to prevent tumour metastasis or inhibit the growth of a primary tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptides having potent anti-angiogenic activity, useful for the treatment of tumors, comprise a portion of a FLT-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anglogenesis; plasminogen; endostatin; Endo-; VEGF; vascultar endothabial growth factor; FLT-1; kinase insert domain; FLK-1; vascultar endothabial growth factor; FLT-1; kinase insert domain; FLK-1; anglogenic inhibitor; Anglo-; endothabial cell; proliferation; tumour growth; blood vessel formation; migration; tubule structure; embryonic development; wound healing; tumour metaetasis; rheumatoid arthritis; psoriasis; anticancer; therapy; antianglogenic therapy; mitogen; tyrosine kinase receptor.
                                                                                                                                                                                                                                                                                                                      Cytostatic; angiogenesis inhibitor; tumour metastasis; tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present sequence is a peptide which is effective in inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Col 15-16; 21pp; English.
                                                                                                                        AAB80862 standard; peptide; 13 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG97539 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                          Angiostatin-derived peptide #19.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-00385442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0099313P.
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                                                                                                                                                                                                                        (first entry)
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OPVLHLVALNTPL 13
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Best Local Similarity 100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                        Unidentified
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                                                                                                                                                                                                                        29-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-MAR-2001
                                                                                                                                                                       AAB80862;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; endothelial cell proliferation inhibitor; collagen XVIII; angiogenesis inhibitor; anti-tumour; cytostatic; antipsoriatic; assotropic; determatological; ophthalmological; vulnerary; antiarteriosclerotic; antidiabetic; haemostatic; contraceptive; ocular angiogenic disease; ahterosclerosis; scleroderma; myocardial angiogenesis; telangiectasia; angiofibroma; wound granulation.
                                                                                                                                                                                                                                                    Isolated endostatin - useful for treating, e.g. angiogenesis dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                      novel 20kDa endostatin that specifically inhibits endothelial cell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94321 standard; peptide; 20 AA
                                                                                                                                                                                                                                                                                           Claim 3; Page 56; 84pp; English
                                                                                                    95US-0005835P.
96US-0023070P.
96US-0026263P.
96US-00740168.
                                                                                                                                                                       (CHIL-) CHILDRENS MEDICAL CENT
                                                                            96WO-US016925
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse endostatin N-terminus,
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                                                                                                                                                                                                Folkman MJ;
                                                                                                                                                                                                                           WPI; 1997-259020/23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 AA;
                       WO9715666-A1
                                                                                                                02-AUG-1996;
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                                                                         23-0CT-1996;
                                                                                                                                             22-OCT-1996;
                                                                                                     23-OCT-1995;
                                                  01-MAY-1997
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Mus sp
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specific procedulations of endomination of the sequence corresponds to a C-terminal fragment of newly identified collagen type XVIII. Recombinant mouse endostatin (20 mg/kg) was administered subcutaneously to mice implanted with Lewis lung carcinomas. There was tumour mass regression non-detectable levels after 12 days of therapy due to the anglogenesis inhibitory activity of endostatin. Thus the protein is useful for treatment of anglogenesis-dependent cancers. The polynucleotide and polypeptide sequences of this endostatin are useful for treating and diagnosis of tumours, ocular anglogenic diseases, Obler-Webber syndrom, myocardial anglogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, anglofibroma and wound garanulation, for treatment of diseases related to excessive or abnormal stimulation of endothelial cells e.g. intestinal adhesions atherosclerosis, scleroderma. The protein may also be useful as a birth control agent by reducing or preventing uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel endostatin capable of inhibiting endothelial cell proliferation and angiogenesis, useful for treating angiogenesis-dependent cancers and as birth control agents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vascularisation. The gene for endostatin may be isolated from cells or tissue that express high levels of endostatin, eg. tumour cells, by generating cDNA from mRNA using reverse transcriptase and then amplifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy; arthritis; wound healing; Helicobacter pylori; peptic ulcer; gene therapy; angiostatin antagonist; endostatin antagonist; antiantiangiogenic; cytostatic; antiarthritic; antiinflammatory; cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary; gynaecological; cat scratch fever.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the N-terminus of an endostatin, a potent and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 2; 68pp; English.
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                                                                                                                                                                                                                                                                                                                         (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endostatin N-terminal peptide.
                                                                                                                                             99WO-US025605
                                                                                                                                                                                                                  98US-0106343P
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                                                                                                                                                                                                                                                                                                                                                                                                  O'reilly MS, Folkman MJ;
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WO200026368-A2
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                                                                                                                                                                                                                                                     20-MAY-1999;
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                                                                                                                                             01-NOV-1999;
                                                                                                                                                                                                                      30-OCT-1998;
                                                                    11-MAY-2000
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The invention relates to an isolated mouse endostatin (potent inhibitor endothelial proliferation). Also include are a compound comprising an isolated mucleic acid sequence encoding the endostatin protein (or an isolated mucleic acid sequence encoding the endostatin protein (or an isolated antibody capable of specifically binding to endostatin protein), treating an angiogenesis-related disease, treating angiogenesis-dependent cancer, a method of birth control, a composition comprising angiostatin and making the endostatin protein. The endostatin is useful for preparing a composition for treating an angiogenesis-related disease, e.g. angiogenesis-dependent cancer, psoriasis, wound granulation or atherosclerosis. Microsequence analysis of the 20 kDa inhibitor of capillary endothelial cell proliferation from the conditioned media ceid N-terminal microsequence analysis of the purified inhibitor of capillary endothelial cell proliferation confirmed that it was identical to a C-terminal fragment of the NCI domain. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  haemangioma; leukaemia; metastasis; telangiectasia; psoriasis; scleroderma; pyogenic granuloma; myocardial angiogenesis; plaque neovascularisation; coronary collateral; arteriovenous malformation; ischaemic limb angiogenesis; corneal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytostatic; vulnerary; vasotropic; antipsoriatic; dermatological; cardiant; ophthalmological; antidiabetic; antiarthritic; antiulcer; osteopathic; gynaecological; contraceptive; endostatin; sucrose octasulfate; angiogenesis inhibitor; endostatin proliferation inhibitor; endostatin biosynthesis; anti-angiogenic compound; collagen type XVIII; endothelial cell-related disorder; angiogenesis related disease; cancer; endothelial cell-related disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibitory fragment of collagen XVIII was named endostatin. The present sequence is the N-terminus of the isolated endostatin.
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                                                             New endostatin, useful for preparing a composition for treating an angiogenesis-related disease, e.g. angiogenesis-dependent cancer, psoriasis, wound granulation or atherosclerosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 66; DB 7; Length 20; 100.0%; Pred. No. 5.7e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                   Claim 3; Fig 5; 35pp; English.
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WPI; 2003-635177/60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              individual by administering an angiogenesis regulating composition comprising a tropomyosin binding compound or an actin disrupting compound. The compositions are useful for treating diseases and processes mediated by angiogenesis including haemangioma, solid tumours, blood bourne tumours, leukaemia, metastasis, Crohn's disease, coronary or cerebral collaterals, arthritis, diabetic neovascularisation, macular degeneration, wound healing, Helicobacter related diseases, ovulation, menstruation, and cat scratch fever. The present sequence is a peptide described in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulating angiogenesis and treatment of angiogenesis-mediated diseases, e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding compound or actin disrupting compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention relates to methods of regulating angiogenesis in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mouse; endostatin; N-terminus; cytostatic; antipsoriatic; vulnerary; antiarterioscolerotic; angiogeneeis-related disease; angiogeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-togeneeis-t
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                                                                                                                                                 04-JUN-2001; 2001WO-US017947.
                                                                                                                                                                                                                       02-JUN-2000; 2000US-0209065P.
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Best Local Similarity luv...
Local 3; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  Sim KL, Macdonald NJ;
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                                                                                                                                                                                                                                                                                                                                (ENTR-) ENTREMED INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2002-130569/17.
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          WO200193897-A2
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The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of premarturity, macular degeneration, corneal graft rejection, of premarturity, macular degeneration, corneal graft rejection, retrolental fibroplasia, rubeosis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include osler-Webber syndrome, myocardial angiogenesis, plaque neovasculisation, telangiectesia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes a number of peptides derived from endostatin which exhibit antiangingenic activity. These may be used in the treatment of cancer. The present sequence is one of the peptides of the invention
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                                                                                                                 Endostatin peptide comprising at least four endostatin amino acid residues are e.g. angiogenesis inhibitors for treating cancer and diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 66; DB 4; Length 23; 100.0%; Pred. No. 6.7e-05; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                  Example 4; Page 124; 146pp; English.
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(UYPI-) UNIV FIRENZE.
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                                                                  WPI; 2001-040937/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 23 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB35584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                    Vuori K;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        요
                                                                                                                                                                                                                                                                             The invention describes a composition comprising endostatin and sucrose octasulfate. Also described are: a new endostatin protein, which is a concasulfate. Also described are: a new endostatin protein, which is a concasulfate. Also described are: a new endostatin protein, which is a proliferation; molecular probes for the ribonucleic acid and decorption and translation of endostatin, molecular probes for the ribonucleic acid sequences comprision uncleotide caces in transcription and translation of sustained release anti-angiogenic compounds; nucleic acid sequences comprision nucleotide codons that code for the endostatin serving as sustained release anti-angiogenic compounds; nucleic acid sequences comprision uncleotide codons that code for the endostatin in protein framents; identification of receptors specific for endostatin; comprision of enzymes capable of releasing endostatin in biological fragments; identification of endothelial cell-related diseases and diseases. The composition and measurement of endostatin in biological fluids and tissues. The composition is useful for treating angiogenesis related diseases including cancer, haemangioma, leuksemia, metastasis, telangiectasia, psoriasis, scleroderma, pyogenic granuloma, myocardial angiogenesis, necessis, plaque neovascularisation, cornary collateral, arthritis, diabetic neovascularisation, macular cibroplasia, arthritis, diabetic neovascularisation, macular cibroplasia, hematopoiesis, ovulation, pactures, keloids, vasculogenesis, hematopoiesis, ovulation, placer, fractures, keloids, cornary contains the amino acid sequence of human endostatin N. cornary contains inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                 Composition useful for treating angiogenesis related diseases e.g. cancer comprises endostatin and sucrose octasulfate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endostatin, antiangiogenic, angiogenesis; human, mouse, chicken, cancer, inflammation, angiogenesis-dependent disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Murine endostatin peptide fragment SEQ ID NO: 19
                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB49806 standard; peptide; 23 AA.
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                   WPI; 2004-374910/35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20 AA;
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                    (YIMZ/) YIM Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus.
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AAB49806;

AAB49806

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Gaps

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Gene clone of inhibitory factor for hyperplasia of inner blood vessel cells in human body's real tumor, and its use in anti-tumor blood vessel
                                                                                                                            Endostatin; murine; proliferation; blood vessel endothelium; regeneration; tumour; blood vessel; treatment; amplification.
                      AAM49504 standard; protein; 183 AA.
                                                                             07-MAY-2002 (first entry)
                                                                                                       Mouse endostatin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-106746/15.
                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                              (xugg/) xu g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regeneration.
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                                                  AAM49504;
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                                                                                                                                                                                                                                                                             Mouse; endostatin; antitumour; cytostatic; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; gene therapy; angiogenic inhibitor; adenoviral vector; diabetic retinopathy; cardiovascular disease; arthritis; psoriasis; cerebral oedema; intravascular coagulopathy; lymphoma; leukaemia; sig-mEndo; fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenoviral vector for treating tumors and disorders associated with angiogenesis, such as cancer, arthritis, and psoriasis, comprises a DNA sequence encoding an angiogenic inhibitor, particularly endostatin.
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                                                   Gaps
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                         Length 39;
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                                                 Indels
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                       Score 66; DB 4; L
Pred. No. 0.00012;
           100.0%; Scor.
100.0%; Pred. No. v..
0; Mismatches
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(NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
                                                                                                                                                                         AAB71931 standard; protein; 42 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-00373938
                                                                                                                                                                                                                            (first entry)
                                                                                              OPVLHLVALNTPL 19
                                                                              1 OPVLHLVALNTPL 13
                                                   13; Conservative
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Matches 13; Conser
                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-AUG-1999;
Sequence 39
                                                                                                                                                                                                                             10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    22-FEB-2001
                                                                                                                                                                                                   AAB71931;
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                          Query Match
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                                                   Matches
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Location/Qualifiers

/label= Ser, Phe

97CN-00107112. 97CN-00107112.

Xu L;

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EMI; anti-angiogenic peptide; endostatin; angiogenesis-dependent cancer; benign tumour; rheumatoid arthritis; psoriasis; ocular angiogenesis; oslar-webber Syndrome; mycardial angiogenesis; angiofibroma; cancer; plaque neovascularisation; telangiectasia; atherosclerosis; scleroderma; dialysis graft vascular access stenosis; renal cancer; therapy.
                                      This invention describes a novel preparation which inhibits the proliferation of blood vessel endothelium and prevents the regeneration activity of tumour blood vessels. The preparation can also be used as a biological preparation in the treatment of tumours. This sequence represents the murine endostatin protein described in the invention
                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                              5; Length 183;
                                                                                                                                                                                                                                                                                             0; Indels
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100.0%; Pred. No. 0.00071;
ive 0; Mismatches 0;
Disclosure; Page 4 (Disclosure); 6pp; Chinese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endostatin protein sequence.
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Matches 13; Conservative
                                                                                                                                                                                                Sequence 183 AA;
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30 QPVLHLVALNTPL 42

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1 QPVLHLVALNTPL 13

(BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.

WPI; 1999-385604/32. N-PSDB; AAX79949

Sukhatme VP;

97US-0067888P. 98US-0082663P. 98US-0108536P.

22-APR-1998;

98WO-US026057

08-DEC-1998; 08-DEC-1997; 16-NOV-1998;

WO9929855-A1

Mus sp.

17-JUN-1999

Claim 31; Fig 2; 105pp; English

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This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine endostatin and angioagenesis-inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells exvivo and then administered to the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine; immunoglobulin Fc fragment; endostatin; immunofusin; anagiogenesis; inhibitor; cytostatic; antirheumatoid; antiarthritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosolerosis; tumour; metastasis; atherosolerosis; psoriasis; rheumatoid arthritis; ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy.
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Pred. No. 0.00071;
Mismatches 0; Indels
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                                                                                               (GENE-) GENETIX PHARM INC.
(MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                        Bachelot T;
                                                                                                                                                                                                                                                                                          Anti-angiogenic gene therapy vectors.
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                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 6; 83pp; English
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1 Similarity 100.0%; P:
13; Conservative 0;
98WO-US024950.
                                                  97US-00975424
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                                                                                                                                                                      Leboulch P, Pawliuk RJ,
                                                                                                                                                                                                                   WPI; 1999-357696/30.
N-PSDB; AAX77715.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 184 AA;
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     20-NOV-1998;
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                                                  20-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is the mouse endostatin. The invention relates to a the mutant endostatin (EM), which has anti-angiogenic activity, and is designated EMI. Compositions comprising EMI or fusion proteins comprising CEMI, are useful for treating diseases characterised by angiogenic activity, such as angiogenesis. General endosterised by angiogenic EMI, are useful for treating diseases characterised by angiogenic comprising cativity, such as angiogenesis, ocular angiogenesis, Osler-Webber Syndrome, myocardial angiogenesis, ocular angiogenesis, Osler-Webber Syndrome, macoratial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, contracted disease, Helicobacter pylori ulcers, dialysis graft vascular access stenosis, contraception and obesity. In particular, the diseases of treatable by EMI comprise cancer, especially renal cancer. The methods provide a means for introducing EMI into mammalian cells via gene therapy, for production of the EMI protein. EMI performs as well as tecombinant production of the EMI protein. EMI performs as well or than whole endostatin. Use of EMI is advantageous for treatment of angiogenic diseases in that increasingly smaller peptides are more potent angiogenic diseases in that increasingly smaller peptides are more potent
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Pred. No. 0.00071;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mutant endostatin having anti-angiogenic activity
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0; Mismatches

100.0%;

Query Match 100. Best Local Similarity 100. Matches 13; Conservative

Sequence 184 AA;

AAY08689 standard; protein; 184 AA.

1 OPVLHLVALNTPL 13

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Murine endostatin protein fragment.

10-AUG-1999

AAY08689;

WO9926480-A1

Mus sp.

03-JUN-1999

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Gaps

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WPI; 2000-237616/20.
N-PSDB; AAZ51299.
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Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration.

Example 5; Page 48-49; 68pp; English.

a lighted dequence, an immunoglobulin Errogion, and an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment chaving angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, consistent tumour metastasis, benign tumours including mediated blood born tumours metastasis, benign tumours including mediated conditions themmandiomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabbetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental confibroma, rubeosis and Osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, or angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in the construction of immunofusin murine immunoglobulin Fc fragment The patent discloses a DNA molecule encoding a fusion protein comprising

Sequence 184 AA;

Gaps ö 100.0%; Score 66; DB 3; Length 184; 100.0%; Pred. No. 0.00071; tive 0; Mismatches 0; Indels Query Match Best Local Similarity 100. Matches 13; Conservative

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1 OPVLHLVALNTPL 13

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Search completed: March 10, 2005, 11:06:51 Job time : 67.0263 secs

7 OPVLHLVALNTPL 19 ద

8209, Ap 4, Appli 2, Appli 12, Appli 20, Appl 5, Appli 5, Appli 1882, A 87, Appli 9, Appli

Title: Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

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Sequence 30, Application US/09385442
| Batent No. 6200954
| Patent No. 6200954
| APPLICANT: No. 6200954
| APPLICANT: Kini, R. Manjunatha
| APPLICANT: Kini, R. Manjunatha
| TITLE OF INVENTION: Small Peptides Having Potent Anti-Angiogenic Activity
| FILE REFERENCE: 1781-170P
| CURRENT FILING DATE: 1999-08-30
| EARLIER FILING DATE: 1999-09-04
| NUMBER OF SEQ ID NOS: 50
| SOFTWARE: Petentin Ver. 2.0
| SEQ ID NO 30
| LENGTH: 13
                                                                                                                                                                                                                    Sequence 9, Appl. Sequence 40331, Sequence 55547,
                                                                     Sequence 1, Assequence 13, A Sequence 20, A Sequence 20, A Sequence 3, Ap Sequence 3, Ap Sequence 81, A
                                                                                                                                                                                                                                                                        Sequence 17,
Sequence 17,
Sequence 17,
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Patent No. (584205)
CENERAL INCORMATION*
O'RELIDY, Michael
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Therapeutic Antiangiogenic Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSE: Jones & Askew, LLP
STREET: 191 Peachtree, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 66; DB 3; Length 13; Best Local Similarity 100.0%; Pred. No. 5.8e-05; Matches 13; Conservative 0; Mismatches 0; Indels
US-09-938-391A-11
US-09-961-403-5
US-09-961-403-5
US-09-938-391A-2
US-09-338-391A-2
US-09-331-077D-12
US-09-331-077D-13
US-09-331-077D-13
US-09-31-077D-13
US-09-389-483-20
US-09-589-483-20
US-09-252-991A-18882
US-09-252-991A-18882
US-09-273-653-87
US-08-273-653-87
US-08-274-653-87
US-09-270-767-40331
US-09-270-767-40331
US-09-270-767-6868-17
US-08-4710-868-17
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US-09-385-442-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30303
COMPUTER READABLE FORM:
   184
684
1516
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ORGANISM: mammalian
   9933.9
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US-09-385-442-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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(/cgn2_6/ptodata1/iaa/5A_COMB.pep:*

(/cgn2_6/ptodata1/iaa/5B_COMB.pep:*

(/cgn2_6/ptodata1/iaa/6A_COMB.pep:*

(/cgn2_6/ptodata1/iaa/6B_COMB.pep:*

(/cgn2_6/ptodata1/iaa/BECOMB.pep:*

(/cgn2_6/ptodata1/iaa/PCTUS_COMB.pep:*

(/cgn2_6/ptodata1/iaa/backfiles1.pep:*
                    GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-315-689-1
US-09-174-282-1
US-09-174-302-1
US-09-105-499-1
US-08-985-56-36
US-09-561-500-13
US-09-561-108-13
US-09-561-499-13
US-09-561-499-13
US-09-561-005-13
US-09-561-69-13
US-09-561-69-13
US-09-561-69-13
US-09-561-689-5
US-09-361-689-5
US-09-361-689-5
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US-09-361-689-5
US-09-361-689-5
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US-09-206-059-2
US-09-938-391A-12
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Maximum Match 100%
Listing first 45 summaries
                                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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66
1 QPVLHLVALNTPL 13
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Maximum DB seq length: 200000000
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Match Length
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Database :

Score

Result No.

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Gaps

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100.0%; Scc.
100.0%; Pre
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FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Murine
ITSSUE TYPE: Collagen
US-09-349-429-1
                                                TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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Best Local Similarity 100.
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Best Local Similarity 100.
Matches 13; Conservative
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                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                     single
                                                                                                                                TYPE: amino acid
STRANDEDNESS: si
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; ORGANISM: murine
US-09-315-689-1
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Sequence 1, Application US/09349429

Patent No. 6174861

GENERAL INFORMATION:

APPLICANT: O'RE111Y, Michael

APPLICANT: Folkman, M. Judah

ITILE OF INVENTION: Therapeutic Antiangiogenic Compositions

TITLE OF INVENTION: and Methods

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 66; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 9.3e-05; Matches 13; Conservative 0; Mismatches 0; Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/740,168A
FILING DATE: 22-OCT-1996
CLASSIFICATION: 536
ATTONEY/AGENT INPORMATION:
NAME: WAZTEN, WIlliam L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0223
TELEPHONE: 404-818-3700
TELEPRAX: 404-818-3700
TELEPRAX: 404-818-3700
TELEPRAX: 404-818-3700
TELEPRAX: 404-818-3700
TELEPRAX: 404-818-3700
TELERAX: 404-818-3700
TELERAX: 404-818-3700
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Jones & Askew, ILP
STREET: 191 Peachtree, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/740,168
FILING DATE: 22-CCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/349,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 30303
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
MCOMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 052
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE: NO FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Murine TISSUE TYPE: Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 OPVLHLVALNTPL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-740-168A-1
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US-03-115-689-1

Sequence 1, Application US/09315689

Patent No. 6346510

GENERAL INFORMATION:

APPLICANT: FOLKman, Judah

TITLE NOT INVENTION: Therapeutic Antiangiogenic Endostatin Compositions

FILE REFRENCE: 05213-0229

CURRENT APPLICATION UNMER: US/09/315,689

CURRENT FILING DATE: 1999-05-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 20
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Sequence 1, Application US/09174282

Sequence 1, Application US/09174282

Patent No. 6544768

PAPLICANT: O'Reilly, Michael

APPLICANT: Polkman, M. Judah

TITLE OF INVENTION: and Methods

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS: 2

CORRESPONDENCE ADDRESS: 374h Floor

STREET: 191 Peachtree, 37th Floor
100.0%; Score 66; DB 3; Length 20; 100.0%; Pred. No. 9.3e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 66; DB 3; Pred. No. 9.3e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA ZIP: 30303 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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Sequence 1, Application US/09174381;
Patent No. 6746865
GENERAL INFORMATION:
APPLICANT: O'S Reilly, Michael
Folkman, M. Judah
TITLE OF INVENTION: Therapeutic Antiangiogenic Compositions
and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/174,381

FILING DATE: 16-Oct-1998

CLASSIFICATION NUMBER: US 08/740,168

FILING DATE: 22-OCT-1996

ATPORNEY/AGENT INFORMATION:

NAME: Warren, William L.

REGISTRATION NUMBER: 36,714

REFERENCE/DOCKET NUMBER: 36,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 66; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS ASKEW, LLP
STREET: 191 Peachtree, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
     05213-0223
                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
:TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
CRGANISM: Murine
TISSUE TYPE: Collagen
US-09-154-302-1
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APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES:
CORRESPONDENCE ABKew, LLP
STREET: 191 Peachtree, 37th Floor
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 66; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 13; Conservative 0; Mismatches 0; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,302
FILING DATE:
CLASSIFICATION NUMBER: US/09/154,302
FILING DATE: 22-OCT-1996
ATPLING DATE: 22-OCT-1996
ATPLING DATE: 22-OCT-1996
ATPORNEY/AGENT INFORMATION:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/174,282
                                                                                                                                                                                                                                                                                                       NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0223
TELECOMUNICATION INFORMATION:
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/740,168
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/09154302
Patent No. 6630448
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REGISTRATION NUMBER: 36,714
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Murine
TISSUE TYPE: Collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                         FILING DATE:
CLASSIFICATION:
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US-09-154-302-1
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Sequence 13, Application US/09561500

Sequence 13, Application US/09561500

Sequence 13, Application US/09561500

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF

TILE REPERENCE: 4001.002500

CURRENT APPLICATION NUMBER: US/09/561,500

CURRENT PILING DATE: 2000-04-28

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR APPLICATION UNDER: 2000-04-28

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 13

LENGTH: 191
                                                               Sequence 36, Application US/08985526

Patent No. 6080728

GENERAL INFORMATION:
TITLE OF INVENTION: CARRIER: DNA COMPLEXES CONTAINING DNA
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
TITLE OF INVENTION: THERAPY
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-561-500-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 66; DB 3; Length 185; 100.0%; Pred. No. 0.001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,526
FILING DATE:
                                                                                                                                                                                                                                                                                     E: Connolly, Bove, Lodge, & Hutz
1220 Market Street, P.O. Box 2207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,845
FILING DATE: 16-UTL-1996
ATTORNEY/AGENT INFORMATION:
NAME: MCMORTOW JT., RODERT G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (302) 658-9141
                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19899
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; FIL
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ORGANISM: Artificial Sequence
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INFORMATION FOR SEQ ID NO:
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Matches 13; Conser
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                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                   US-08-985-526-36
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US-08-985-526-36
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US-09-561-500-13
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Patent No. 6803211
GENERAL INCORMATION:
TAPLICANT: Pfizer, Inc. and Pfizer Products, Inc.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING DISORDERS
TITLE OF INVENTION: INVOIVING ANGIOGENESIS
TITLE OF INVENTION: INVOIVING ANGIOGENESIS
TITLE REFERENCE: 313.00234/PC10799A
CURRENT APPLICATION NUMBER: US/09/938,391A
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 3.2
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Sequence 1, Application US/09405499;
Patent No. 6764995;
GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
APPLICANT: O'Reilly, M. Judah
TITLE OF INVENTION: Endostatin Protein and Fragments Thereof
FILE REFERENCE: 05213-0640
CURRENT APPLICATION WUMBER: US/09/405,499
CURRENT FILING DATE: 1999-09-23
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 20
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                                                                                                                                                                 Length 20
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100.0%; Score 66; DB 4; 1
Best Local Similarity 100.0%; Pred. No. 9.3e-05;
Matches 13; Conservative 0; Mismatches 0;
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                                            ORGANISM: Murine
TISSUE TYPE: Collagen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                            OPVLHLVALNTPL 19
                                                                                                                                                                                                                                                            1 QPVLHLVALNTPL 13
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Matches 13, Conservative
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US-09-405-499-1
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LENGTH: 184
TYPE: PRT
                                                                                                                   US-09-174-381-1
                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-405-499-1
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Gaps

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Sequence 13.
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Sequence 13, Application US/09998831

Sequence 13, Application US/09998831

Septent No. 6676941

SEPERAL INFORMATION:

APPLICANT: Philip E Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: INHIBITING VEGF

TITLE OF INVENTION: INHIBITING VEGF

FILE REFERENCE: 4001.002584

CURRENT PILING DATE: 2001-11.30

FRIOR APPLICATION NUMBER: 09/561,108

PRIOR PILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 191
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-998-831-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-561-499-13
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100.0%; Pred. No. 0.0011;
tive 0; Mismatches 0; Indels
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 13; Conservative
                            US-09-561-499-13
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                                                                                                                                                                                                                                              US-09-561-108-13
Sequence 13, Application US/09561108
Sequence 13, Application US/09561108
Sequence 13, Application US/09561108
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 13, Application US/09561526
; Sequence 13, Application US/09561526
; Patent No. 6416758
; GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002586
; CURRENT APPLICATION NUMBER: US/09/561,526
; CURRENT FILING DATE: 1090-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 13
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC WS-09-561-108-13
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-561-526-13
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Query Match 100.0%; Score 66; DB 3; Length 191; Best Local Similarity 100.0%; Pred. No. 0.0011; Matches 13; Conservative 0; Mismatches 0; Indels
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GenCore version 5.1.6
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OM protein - protein search, using sw model

March 10, 2005, 10:55:58; Search time 55.8684 Seconds (without alignments) 76.150 Million cell updates/sec Run on:

US-09-766-412-29 59

1 SPHNSYIVLPI 11 Sequence:

Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1990s:*
geneseqp2000s:*
geneseqp2000s:*
geneseqp2001s:*
geneseqp2001s:*
geneseqp2003ss:*
geneseqp2003bs:* A_Geneseq_16Dec04:* 1: genesecro19Rn=.* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Aab74255 Exemplary	Aab80861 Angiostat	Abg97538 Antiangio	Abu20188 Protein e	Aab49808 Murine en	Aab35587 Antiangio	Abp03487 Human ORF	Aam49504 Mouse end	Aay18409 Endostati	Aay08689 Murine en	80	Aab49380 Murine en	Abg31793 Human end	Abu64290 Murine en	Aab28398 Murine en	_	Abj25793 Aspergill		_	Aab71930 Murine en	Abb79902 Mouse end	Adn00602 Murine en	Ado43904 Amino aci	Aay08691 Murine ge	Adh87724 Enterococ
COLEMANTOS	ΙD	AAB74255	AAB80861	ABG97538	ABU20188	AAB49808	AAB35587	ABP03487	AAM49504	AAY18409	AAY08689	AAY70258	AAB49380	ABG31793	ABU64290	AAB28398	AAU77950	ABJ25793	ABJ26393	AAE02031	AAB71930	ABB79902	ADN00602	ADO43904	AAY08691	ADH87724
	DB	4	4	Ŋ	9	4	4	Ŋ	S	7	7	m	4	ഹ	7	m	S	9	9	4	4	S	œ	œ	7	7
	Query Match Length DB	11	11	11	638	48	20	28	183	184	184	184	184	184	184	191	191	201	201	207	207	207	207	207	218	231
de	Query Match	100.0	100.0	100.0	67.8	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1
	Score	59	59	59	40	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39	39
	Result No.		7	٣	4	2	9	7	α0	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

, Aau33460 Enterococ Abu44591 Protein e	Aau35185 Enterococ Abu14632 Protein e	Aay08692 Murine ge	_		Aaw92297 Mouse alp	Abo84585 Mouse can	Abo84584 Mouse can	Abb61083 Drosophil	Ads43599 Bacterial	Abo83463 Pseudomon	Abu21359 Protein e	Adb09837 Alloiococ	Abu33803 Protein e	Abu34059 Protein e	Abu36425 Protein e	Abu34704 Protein e	Aao17569 M catarrh
AAU33460 ABU44591	AAU35185 ABU14632	AAY08692	AAY25114	AAW26328	AAW92297	AB084585	AB084584	ABB61083	ADS43599	AB083463	ABU21359	ADB09837	ABU33803	ABU34059	ABU36425	ABU34704	AA017569
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455 466	472	580	684	1288	1288	1315	1527	1987	818	441	628	123	227	245	264	265	289
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99	99	99	99	66.1	99	99	99	99	65.3	64	64	62	62	62	62	62.7	62
39 39	თ ი ო ო	39	39	39	39	39	39	39	38.5	38	38	37	37	37	37	37	37
26 27	28 29	30	31	32	33	34	35	36	37	38	. 68	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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The present invention relates to anti-angiogenesis peptides from a portion of a selected from plasminogen, endostatin, VEGF or FLT-1. The invention is used to prevent or treat primary tumour growth or metastasis or undesired angiogenesis
                                                                                                                  Anti-angiogenesis; plasminogen; VEGF; vascular endothelial growth factor; FLT-1; tumour; metastasis; cancer.
                                                                                                                                                                                                                                                                                                                                                                        Peptides comprising a portion of a protein selected from plasminogen, endostatin, VEGF, FLT-1 and KDR/FLK-1 are useful for treating primary tumor growth.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 59; DB 4; Length 11; Best Local Similarity 100.0%; Pred. No. 0.00029; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                          Exemplary anti-angiogenic peptide #29.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 7; Page 18; 34pp; English.
           AAB74255 standard; peptide; 11
                                                                                                                                                                                                                                          01-SEP-2000; 2000WO-SG000131.
                                                                                                                                                                                                                                                                   99SG-00004310.
                                                                                                                                                                                                                                                                                            (UYSI-) UNIV SINGAPORE NAT.
                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                               WPI; 2001-257785/26.
                                                                                                                                                                                     WO200118030-A2.
                                                                                                                                                                                                                                                                                                                      Ge R, Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11 AA;
                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                   03-SEP-1999;
                                                              23-MAY-2001
                                                                                                                                                                                                              15-MAR-2001.
                                     AAB74255;
AAB74255
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1 SPHNSYIVLPI 11

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides having potent anti-angiogenic activity, useful for the treatment of tumors, comprise a portion of a FLT-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Angiogenesis; plasminogen; endostatin; Endo-; VEGF; vascular endothabial growth factor; FLT-1; kinase insert domain; FLK-1; angiogenic inhibitor; Angio-; endothelial cell; proliferation; tumour growth; blood vessel formation; migration; tubule structure; embryonic development; wound healing; tumour metastasis; rheumatoid arthritis; psoriasis; anticancer; therapy; anticancer; antiangiogenic therapy; mitogen; tyrosine kinase receptor.
                                                                                                                                                                                               Cytostatic; angiogenesis inhibitor; tumour metastasis; tumour growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 59; DB 4; I 100.0%; Pred. No. 0.00029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Col 15-16; 21pp; English.
                                                                        AAB80861 standard; peptide; 11 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABG97538 standard; peptide; 11 AA.
                                                                                                                                                                  Angiostatin-derived peptide #18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiangiogenic peptide, Endo-1.
                                                                                                                                                                                                                                                                                                                   99US-00385442
                                                                                                                                                                                                                                                                                                                                                 98US-0099313P
                                                                                                                                                                                                                                                                                                                                                                            (UYSI-) UNIV SINGAPORE NAT
                                                                                                                                   29-MAY-2001 (first entry)
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Best Local Similarity 100.
Matches 11; Conservative
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1 SPHNSYIVLPI 11
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                                                                                                                                                                                                                                                                                                                                                                                                            Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 11 AA;
                                                                                                                                                                                                                                                         US6200954-B1
                                                                                                                                                                                                                                                                                                                                                 04-SEP-1998;
                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                   30-AUG-1999;
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                                                                                                                                                                                                                                                                                       13-MAR-2001
                                                                                                      AAB80861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG97538;
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                                                       AAB80861
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The invention discloses a peptide comprising a portion of a protein e.g. plasminogen, endostatin (Endo-1-4), vascular endothelial growth factor (VEGE); FIL-1 or kinase insert domain containing receptor/FEK-1. These peptides are able to act as potent angiogenic inhibitors (Angio-1-5) inhibiting endothelial cell proliferation and retarding tumour growth. CC Angiogenesis is the process of new blood vessel formation from precessing the process of new blood vessel formation from precessing the process of new blood vessel formation from precessing the total structures. It plays an important role in normal physiological functions such as embryonic development and wound healing. Inappropriate angiogenesis is also associated with various pathological conditions including tumour growth and metestasis, rheumatcid arthritis and psoriasis Anticancer therapy by inhibiting tumour angiogenesis is called antiangiogenic therapy by inhibiting tumour angiogenesis is that functions through two high affinity tyrosine kinase receptors, FLT-1 and FLK-1 (not defined). Protein-protein interactions are crucial to many physiological undesired angiogenesis and the peptides disclosed interafing undesired angiogenesis and primary tumour growth or metastasis. The sequences presented in ABG97510-ABG97559 are examples of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                         portion of a protein e.g. plasminogen, endostatin, and potent antiangiogenic activity and endothelial cell proliferation inhibition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                        Novel peptide for preventing/treating undesired angiogenesis, has
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein encoded by Prokaryotic essential gene #5715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU20188 standard; protein; 638 AA.
                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Page 9; 24pp; English.
                                                                                      22-JAN-2001; 2001US-00766412.
                                                                                                                       98US-0099313P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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                                                                                                                                                                                                                                                                    WPI; 2002-749595/81.
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                                                                                                                                                                          (GERR/) GE R.
(KINI/) KINI R M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Borrelia cepacia.
              US2002103129-A1.
                                                                                                                                                                                                                                  Kini RM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200277183-A2.
                                                                                                                         04-SEP-1998;
                                                                                                                                        30-AUG-1999;
                                                  01-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                          activity.
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                                                                                                                                                                                                                                Ge R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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ų, Wang Wall

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the modulation of anglogenesis. This is useful in the treatment of cancers, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of vessels such as diabetic retinopathy, neovascular glaucoma, retinopathy of prematurity, macular degeneration, corneal graft rejection, retrolental fibroplasia, rubeosis, capillary proliferation in atheroselerotic plaques and osteoporosis. Other anglogenesis-dependent diseases include Osle-Webber syndrome, myocardial anglogenesis, plaque neovasculisation, telangiectasia, haemophilac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                          Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken; cancer; inflammation; angiogenesis-dependent disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides endostatin peptides which can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Endostatin peptide comprising at least four endostatin amino acid residues are e.g. anglogenesis inhibitors for treating cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39; DB 4; Length 48;
Pred. No. 9.2;
0; Mismatches 2; Indels
                           Murine endostatin peptide fragment SEQ ID NO: 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 10; Page 124-125; 146pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antiangiogenic pentacontapeptide IV.
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                                                                                                                                                                                                                                                                                                                                                                  99US-0132907P.
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81.8%;
                                                                                                                                                                                                                                                                                                                02-MAY-2000; 2000WO-US012063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 48 AA;
                                                                                                                                                                                                           WO200067771-A1.
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                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1999;
14-JUL-1999;
                                                                                                                                                         Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-OCT-2000.
                                                                                                                                                                                                                                                            16-NOV-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated mucieic acid comprising any one or the following an interest sequences given in the specification where expression of the nucleic acid inhibites proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense continuous properties or its fragment whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated continuous continuous cardinal continuous cardinal continuous cardinal continuous cardinal continuous cardinal 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fig. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              one of
                                                                                                                                                                                                                                                                                     Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid comprising any the 6213 antisense sequences given in the specification where exp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                     Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                               Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 25; SEQ ID NO 48112; 1766pp; English.
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                                                                                                                                                                                                                                                                                  Malone C,
Carr GJ,
                                                                 21-MAR-2001; 2001US-00815242.
06-SEP-2001; 2001US-0094893.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-03072851.
06-MAR-2002; 2002US-0362699P.
                21-MAR-2002, 2002WO-US009107
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                                                                                                                                                                                                                              (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 TPHLSHLVLPI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 SPHNSYIVLPI 11
                                                                                                                                                                                                                                                                               Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                               2003-029926/02
                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-029926,
N-PSDB; ACA24058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 638 AA;
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Gaps

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AAB49808;

SXXXE

RESULT 5 AAB49808

Query Match

Best Loc Matches

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The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABMISTAGE cancode the human ORFX proteins given in ABPO0010 to ABPISTO. ORFX proteing are useful for reating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a squences can be used in gene therapy. ORFX sequences can be used in gene therapy. ORFX sequences can be used in the sequences can be used in gene therapy. ORFX sequences can be used in the squences can be used in gene therapy. ORFX sequences can be used in the squences can be used in gene therapy. ORFX sequences can be used in the sequences can be used in the securation to cardiovascular disorders, disorders nearly the corganisms, benign tumours, keloid, degenerative disorders, haemorrhage, osteoarthritis, neurodegenrative disorders, disorders related to organ transplantation, cardiovascular diseases, diabetes mallitus, systemic truchmmune disorders such as multiple sclerosis, rheumatoid diseases, and autoimmune thyroiditis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eve disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bene degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence date for this patent did not form part of the printed specification, but was obtained in electronic form at directly from WIPO at fip.wipo.int/published_pot_gequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene clone of inhibitory factor for hyperplasia of inner blood vessel cells in human body's real tumor, and its use in anti-tumor blood vessel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Endostatin; murine; proliferation; blood vessel endothelium; regeneration; tumour; blood vessel; treatment; amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ŝ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 5
Pred. No. 11;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAM49504 standard; protein; 183 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97CN-00107112.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse endostatin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu L;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-106746/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 58 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ren M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             regeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (xugg/) xu g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN1177005-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAM49504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; myasthenia gravis.
                                                                                                                                                                                                                                                                                                                              The present invention describes a number of peptides derived from endostatin which exhibit antiangiogenic activity. These may be used in the treatment of cancer. The present sequence is one of the peptides of the invention
                                                                                                                                                                                                                     Polypeptides derived from endostatin exhibiting antiangiogenic activity useful for treatment of angiogenesis-dependent tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel human polypeptides and polynuclectides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 4; Length 50;
Pred. No. 9.6;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ORFX protein sequence SEQ ID NO:6956.
                                                                                                                                  Ξ
                                                                                                                                  Ziche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABP03487 standard; protein; 58 AA.
                                                                                                                                                                                                                                                                                            Claim 5; Page 18; 28pp; English.
                     99IT-MI000777.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 81.8%;
Matches 9; Conservative
                                                                                                                                    Francescato P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SPHNSYIVLPI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 SCHNSYIVLCI 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimkets RA, Leach MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-106308/14.
                                                                                     (UYFI-) UNIV FIRENZE
                                                                                                                                                                             WPI; 2001-007005/01.
                                                                (UYMI-) UNIV MILANO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ABN19239
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200192523-A2
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                  15-APR-1999;
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                                                                                                                                Chillemi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-2001
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RESULT 7 ABP03487

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Length 58; 1; Indels

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Disclosure; Fig 6; 83pp; English
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0
                                                                          66.1%;
81.8%;
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81.8%;
                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Leboulch P, Pawliuk RJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 81.8
                                                                                                      9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                164 SCHNSYIVLCI 174
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                                                                                                                              1 SPHNSYIVLPI 11
                                                                                                                                                     164 SCHNSYIVLCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SPHNSYIVLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-357696/30.
                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAX77715
                                                   Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184 AA;
                                                                                                                                                                                                                                                                         10-AUG-1999
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Best Local S
                                                                                                                                                                                                                                                 AAY08689;
                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                 Mus sp.
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                                                                                                      Matches
                                                                                                                                                                                              RESULT 10
AAY08689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            activity, such as not ceating unsease intracterists by autogenic activity, such as not openesis dependent cancers, benign tumours, rheumatoid arthritis, psoriasis, ocular angiogenesis, obler Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, telangiectesia, haemophiliac joints, angiofibroma, wound granulation, intestinal adhesions, atherosclerosis, scleroderma, hypertrophic scars, cat scratch disease, Helicobacter pylori ulcers, dialysis graft vascular access stenosis, contraception and obesity. In particular, the diseases treatable by EMI comprise cancer, especially renal cancer. The methods provide a means for introducing EMI into mammalian cells via gene therapy, for production of EMI via recombinant means, as well as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence is the mouse endostatin. The invention relates to a the mutant endostatin (EM), which has anti-angiogenic activity, and is designated EM1. Compositions comprising EM1 or fusion proteins comprising EM1, are useful for treating diseases characterised by angiogenic
                                                                                                                                                                                                                                                                                                                                                                             EM1; anti-angiogenic peptide; endostatin; angiogenesis-dependent cancer; benign tumour; rheumatoid arthritis; psoriasis; ocular angiogenesis; osler-Webber Syndrome; mycardial angiogenesis; angiofibroma; cancer; plaque neovascularisation; telangiectasia; atherosclerosis; scleroderma; dialysis graft vascular access stenosis; renal cancer; therapy.
                     This invention describes a novel preparation which inhibits the proliferation of blood vessel endothelium and prevents the regeneration activity of tumour blood vessels. The preparation can also be used as a biological preparation in the treatment of tumours. This sequence represents the murine endostatin protein described in the invention
                                                                                                                                                        Gaps
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                                                                                                                              DB 5; Length 183;
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mutant endostatin having anti-angiogenic activity
Disclosure; Page 4 (Disclosure); 6pp; Chinese.
                                                                                                                             Score 39; DB 5
Pred. No. 41;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                                                                                                                                                                                                                                                                        AAY18409 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 31; Fig 2; 105pp; English
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98US-0082663P.
98US-0108536P.
                                                                                                                          Similarity 81.8%;
9; Conservative C
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                                                                                                                                                                                                                                                                                                                                                     Endostatin protein sequence.
                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                       164 SCHNSYIVLCI 174
                                                                                                                                                                                1 SPHNSYIVLPI 11
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N-PSDB; AAX79949.
                                                                                                                            Ouery Match
Best Local Similarity
Matches 9; Conserv
                                                                                                      Sequence 183 AA;
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16-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sukhatme VP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus sp.
                                                                                                                                                                                                                                             RESULT 9
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                                         more potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasminogen, murine; angiostatin, endostatin, gene therapy, vector; anti-angiogenic; attenuation, cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina.
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
than whole endostatin. Use of EMI is advantageous for treatment of angiogenic diseases in that increasingly smaller peptides are more on a weight basis, and may be able to better penetrate tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .;
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                                                                                                                                                                                                                       Length 184;
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Pred. No. 42;
0; Mismatches
                                                                                                                                                                                                                           Score 39; DB 2;
Pred. No. 42;
                                                                                                                                                                                                                                                                                                  0; Mismatches
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(MASI ) MASSACHUSETTS INST TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bachelot T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-angiogenic gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Murine endostatin protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY08689 standard; protein; 184 AA.
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AAB49380 standard; protein; 184 AA.

RESULT 12

AAB49380

Murine endostatin SEQ ID NO: 4.

(first entry)

02-MAR-2001

AAB49380;

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The patent discloses a DNA molecule encoding a fusion protein comprising a signal sequence, an immunoglobulin Fc region, and an angiogenesis influitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours, tumour metastasis, benign tumours including haemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic panniomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases e.g. diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis and Osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints, angiofibroma, wound granulation, and excessive or abnormal stimulation of endothelial cells, intestinal cells, atherosclerosis, sclerodermal and hypertrophic scars, i.e. kelodid scars, the DNA constructs may be used in the construction of immunofusin murine immunoglobulin Fc fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel fusion protein of angiostatin or endostatin and an immunoglobulin FC region, useful for treating conditions mediated by angiogenesis, such as rheumatoid arthritis, tumors and macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                   Murine, immunoglobulin Fc fragment, endostatin, immunofusin, angiogenesis; inhibitor; cytostatic, antitheumatoid, antiarthritic; antidiabetic; ophthalmological; immunosuppressant; vasotropic, vulnerary, treatment, antiarteriosclerosis; tumour, metastasis; atherosclerosis; psoriasis; rheumatoid arthritis; collar angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy.
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Pred. No. 42;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                      Murine angiogenesis inhibitor, endostatin.
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                                                                              AAY70258 standard; protein; 184 AA.
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                                                                                                                                                                                                                                               (first entry)
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N-PSDB; AAZ51299.
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Best Local Similarity
Matches 9; Conserv
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of premarturity, macular degeneration, corneal graft rejection, retrolental fibroplasia, rubosats, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include osler-Webber syndrome, myccardial angiogenesis, plaque neovasculisation, telangiectasia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                              Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken; cancer; inflammation; angiogenesis-dependent disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                              Endostatin peptide comprising at least four endostatin amino acid residues are e.g. angiogenesis inhibitors for treating cancer and diabetic retinopathy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 4; Length 184;
Pred. No. 42;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 1; 146pp; English.
                                                                                                                                                                                                                            02-MAY-2000; 2000WO-US012063.
                                                                                                                                                                                                                                                        99US-0132907P.
                                                                                                                                                                                                                                                                     99US-00353333.
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81.8%;
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Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                 (BURN-) BURNHAM INST.
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                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-040937/05.
                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAC88290.
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                                                                                                                                                                     WO200067771-A1.
                                                                                                                                                                                                                                                      06-MAY-1999;
14-JUL-1999;
                                                                                                                                          Mus musculus.
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The present invention relates to an adeno-associated viral (AAV) vector comprising a polynucleotide that comprises a nucleic acid segment that encodes a choroidal or ocular neovascularisation inhibitory polypeptide operably linked to a promoter that expresses the segment to produce the polypeptide in a selected mammalian host cell. Such a vector is useful for providing a choroidal or ocular neovascularisation inhibitory polypeptide to a mammal, for use in the therapy of ocular neovascularisation, age-related macular degeneration, retinal neovascularisation, age-related macular degeneration, visual impairment, ocular dysfunction, loss of vision, retinopathy, or blindness in a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to anti-Vascular Endothelial Growth Factor (VEGF) antibodies that bind to the same epitope as the monoclonal antibody ATCC PTA 1595 and which significantly inhibit VEGF binding to
                                                    Novel adeno-associated viral vector comprising polynucleotide encoding pigment epithelium-derived factor, useful for treating choroidal neovascularization, blindness, loss of vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenic composition for the treatment and diagnosis of cancer comprises an anti-VEGF (vascular endothelial growth factor) antibody binding the same epitope as the monoclonal antibody ATCC PTA 1595.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 7; Length 184;
Pred. No. 42;
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                                                                                                                               Claim 14; Page 38; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.1%;
81.8%;
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N-PSDB; AAC67777.
2003-779243/73.
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                 N-PSDB; AAL56259
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 184 AA;
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                                                                                                                                                                                                                                                                                                                                                      New peptide useful for the preparation of medicaments with antiangiogenic activity that may be used in treating tumors or metastases, comprises a sequence corresponding to fragments of human endostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to peptide comprising 20-50 amino acids with sequences corresponding to the human endostatin polypeptide sequence, its salt or non-toxic derivative. The peptides are useful in the preparation of medicaments with antiangiogenic activity which may be useful in treating tumours or metastases. This sequence represents a human
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Human; endostatin; tumour; cancer; metastasis; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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Pred. No.
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(UYJO ) UNIV JOHNS HOPKINS.
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                                                                                                                                                                  27-FEB-2002; 2002WO-IT000119
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81.8%;
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Best Local Similarity 81.8
Matches 9; Conservative
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                   antiangiogenic
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                                                      Homo sapiens.
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                                                                                                                                                                                                                                                                                 Chillemi F,
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                                                                                                                               06-SEP-2002
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CC the VEGF receptor VEGFR2, without inhibiting VEGF binding to the VEGF creeptor VEGFR1. The present sequence is murine endostatin. Endostatin CC may be conjugated onto the anti-VEGF antibodies of the present invention. CC The anti-VEGF antibodies of the present invention are useful for the CC treatment and diagnosis of cancer, especially vascularised solid tumours XX XX SQ Sequence 191 AA;

Query Match

Query Match

Best Local Similarity 81.8*; Pred. No. 43;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Search completed: March 10, 2005, 11:06:50 Job time : 57.8684 secs

1 SPHNSYIVLPI 11 | | | | | | | | | 171 SCHNSYIVLCI 181

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SEQUENCE FROM N.A.
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NÇBI_TaxID=10090;
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Q9CRT2
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127.183 Million cell updates/sec
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                                                                                                 March 10, 2005, 10:59:54 ; Search time 56.3684 Seconds
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Q6p1y4
P39061
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Q8n4s4
Q6rz41
P39060
Q6rz40
Q6rz40
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Q8awc6
Q83v30
Q9tzf8
Q6ftp7
Q6ftp7
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Q8qh19
Q7rz49
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P54886
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             5.1.6
Compugen Ltd
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             version :
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Q9NA34
P5CS_HUMAN
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CA1H_MOUSE
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Maximum Match 100%
Listing first 45 summaries
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                                                                      protein search, using sw model
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Q8NG19
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Q6RZ41
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Q6RZ40
093419
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Q8AWC6
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Q9QZD2
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             GenCore (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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length: 2000000000
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68
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Perfect score:
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        Q92110 m delta 1-p

        33
        41
        60.3
        795
        2
        Q8BGM2
        Q8bgm2 mus musculu

        34
        41
        60.3
        1348
        2
        Q8FR36
        Q8Fr36
        Q8Fr36 corynebacte

        35
        41
        60.3
        1348
        2
        Q8FR15
        Q8Fr36 corynebacte

        36
        40
        58.8
        270
        Q8FR16
        Q98rys
        rhyzopertha

        39
        40
        58.8
        270
        Q8FRES
        Q94rys
        rhyzopertha

        40
        58.8
        379
        2
        Q8FRES
        Q94rys
        rhyzopertha

        41
        40
        58.8
        432
        2
        Q8FRES
        Q94rys
        rhyzopertha

        42
        40
        58.8
        468
        2
        Q94FS
        Q94rys
        Q94rys

        43
        40
        58.8
        468
        2
        Q94FS
        Q94SS
        P96758
        P96758

        44
        40
        58.8
        468
        2
        Q8G88
        Pr1
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ALIGNMENTS

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OCCURATE PRELIMINARY; PRT; 160 AA.

DO GORTZ

DO GORTZ

DO GORTZ

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DO GORTZ

OL-UNY-2001 (TERBELE-1.17, Created)

OL-UNY-2001 (TERBELE-1.17, Cast sequence update)

OL-UNAR-2004 (TERBELE-1.17, Cast sequence update)

OL-UNAR-2004 (TERBELE-1.26, Last amoreation update)

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Gaps

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Length 171; Indels

RAHARAH KARAHARAH KARAHARA

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley;
STRAIN=Sprague-Dawley;
MEDLINE=20227226; PubMed=10766159;
MEDLINE=20227226; PubMed=10766159;
MEDLINE=0. Concarl P., Giardini R., Marras E., Piccinini F.,
Folkman J., Chen L.;
"Antitumor activity of endostatin against carcinogen-induced rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 68; DB 2; Length 226; 100.0%; Pred. No. 0.00063; ive 0; Mismatches 0; Indels
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171 171
171 AA, 18933 MW, 81BE2EE3FC2C8B72 CRC64,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
11-MAY-2004 (TrEMBLrel. 26, Last annotation update)
Collagen XVIII (Fragment).
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                                                                                                                           100.0%; Score 68; DB 2; I
100.0%; Pred. No. 0.00046;
tive 0; Mismatches 0;
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MGD, MGI:88449, Coll5a1.
GO, GO:0005737, C:cytoplasm; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P3061; IDY1.
InterPro; IPR010515; Endostatin.
Pfam; PF06482; Endostatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primary mammary tumors.";
Cancer Res. 60:1793-1796 (2000)
EMBL; AF189709; AAF00975.1; -.
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Best Local Similarity 100....
Best Ar Conservative
                                                                                                                                                                                                                                                          1 VPIVNLKDEVLSPS 14
                                                                                                                                                                                                                                                                                                                 61 VPIVNLKDEVLSPS 74
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                                                                                                                                                                                            Conservative
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Mus musculus (Mouse).
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nes 14; Conserv
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SEQUENCE
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Adachi J., Aizawa K., Akahira S., Eukudishi Y., Furuno M.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hirancco K., Hiracka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Sano H., Sasaki D., Shibata Y., Shinata Y., Shanishi F., Tanaka T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Muramatsu M., Hayashizaki Y.,
A Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
Muramatsu M., Hayashizaki Y.,
Bubited (Jul-2000) to the EMBL/GenBank/DDBJ databases.
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J. Hepatol. 35:386-331(2001).
HSSP; P39061; 1DYI.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J. Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rira M., Inoue Y., Kira A., Hayashizaki Y.; sequencing pipeline with 384 multicapillary sequencer.";
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'MGI:88451; Coll881.

GO:0005604; C:basement membrane; IDA.
GO:0005615; C:extracellular space; TAS.
GO:0001525; P:angiogenesis; IMP.
GO:0001886; P:endothellal cell morphogenesis; IDA.
GO:0003035; P:positive regulation of apoptosis; IDA.
GO:0030315; P:positive regulation of cell migration; IDA.
GO:0008284; P:positive regulation of cell migration; IDA.
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Collagen type XVIII, alpha (I) chain (Fragment)
Name=coll8a1;
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Pfam; PF06482; Endostatin; 1.
Collagen.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF06482; Endostatin; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VPIVNLKDEVLSPS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45 VPIVNLKDEVLSPS 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 14; Conservative
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                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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RESULT 2 Q9WUW5

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Gaps

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InterPro; IPR010515; Endostatin.
                                               Collagen.
                                                      SEQUENCE
                                                                                                                                                                 Q6P1Y4;
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                                                                                      Matches
                                                                                                                                        RESULT 6
Q6P1Y4
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                                                                                                    Gaps
                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                   100.0%; Score 68; DB 2; Length 1140; 100.0%; Pred. No. 0.0036; ive 0; Mismatches 0; Indels (
                                                     Collagen.
NON TER 1 1 1 SEQUENCE 1140 AA; 115156 WW; 8B0C7E6862B3BDFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                              05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Procollage, type XVIII, alpha 1. Name=Collaga; Mouse) Mouse (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                         PRT; 1315 AA.
GO; GO:0006817; P:phosphate transport; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR008985; ConA_like_lec_gl
                                                                                                                                                                                        05-JUL-2004 (TrEMBLrel. 27, Created)
     InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR010515; Endostatin.
Pfam; PF01391; Collagen; B.
Pfam; PF0482; Endostatin; 1.
ProDom; PD000007; Clg_helix; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                1025 VPIVNLKDEVLSPS 1038
                                                                                                                   1 VPIVNLKDEVLSPS 14
                                                                           Query Match
Best Local Similarity 10v...
                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
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                                                                                                                                                         RESULT 5
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TISSUE-Embryo;

MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

MEDLINE-2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;

A Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Lischul S.F., Zeebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdein T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdein T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Brownstein M.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Shevchenko Y., Bouffard G.G.,

Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield W.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

Rodriguez A.C., Grimwood J., Schner E.D., Dickenson R.C.,

Rodriguez A.C., Grimwood J., Schner B.D., Dickenson R.C.,

Rodriguez A.C., Grimwood J., Schner B.D., Dickenson R.C.,

Rodriguez A.C., Grimwood J., Schner R.D.,

Rodriguez A.
                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=ColiBal;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC064817; AAH64817.1; -.
GO; GO:0005604; C:basement membrane; .IDA.
GO; GO:00018615; C:extracellular space; TAS.
GO; GO:0001865; P:engiogenesis; IMP.
GO; GO:0001886; P:endiothelial cell morphogenesis; IDA.
GO; GO:0043065; P:positive regulation of apoptosis; IDA.
GO; GO:002884; P:positive regulation of cell migration; IDA.
                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                 100.0%; Score 68; DB 2; Length 1315; 100.0%; Pred. No. 0.0042; Live 0; Mismatches 0; Indels (
                                                                                                                                                                              1315 AA; 134245 MW; 15C862C1E385F03A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Procollagen, type XVIII, alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1315 AA
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InterPro; IPR008160; Collagen.
InterPro; IPR008985; ConA like lecgl.
InterPro; IPR010515; Endostatin.
InterPro; IPR010515; Endostatin.
                                                                                     ProDom; PD000007; Clg helix;
SMART; SM00210; TSPN; 1.
                                      Pfam; PF01391; Collagen; 7.
Pfam; PF06482; Endostatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                     1200 VPIVNLKDEVLSPS 1213
IPRO03129; TSP_N.
                                                                                                                                                                                                                                                                                                                                                    1 VPIVNLKDEVLSPS 14
                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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U34609;
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EMBL;
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EMBL;
EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oh S.P., Kamagata Y., Muragaki Y., Timmons S., Ooshima A., Olsen B.R., "Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Kaa-Yaa repeats identify a distinct family of collagenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 3).
STRAIN=BABL5/C; TISSUB=Liver;
STRAIN=BABL5/C; TISSUB=Liver;
MEDLINE=94245707; PubMed=8188673;
Rehn M.V., Hintikka E., Pihlajaniemi T.;
Rehn M.V., Hintikka E., Pihlajaniemi T.;
"Primary Etructure of the alpha 1 chain of mouse type XVIII collagen,
partial structure of the corresponding gene, and comparison of the
alpha 1(XVIII) chain with its homologue, the alpha 1(XV) collagen
                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=96435922; PubMed=8838808; DOI=10.1006/geno.1996.0139;
READ M., Hintikka E., Pihlajaniemi T.;
"Characterization of the sequence gene for the alpha-1 chain of type XVIII collagen (COLIBAL) reveals that the three variant N-terminal polypeptide forms are transcribed from two widely separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  разоба; Q60672; Q61437; Q62001; Q62002; Q3VK63; Q1-FEB-1995 (Rel. 31, Created) 10-OCT-2003 (Rel. 42, Last sequence update) 25-OCT-2004 (Rel. 45, Last annotation update) Collagen alpha I (XVIII) chain precursor [Contains: Endostatin] Name=Coll8al;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=95181468; PubMed=7876242; DOI=10.1074/jbc.270.9.4705;
                                                                                                                                                                                                                  Length 1315;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-562 FROM N.A. (ISOFORMS 1 AND 3), AND TISSUE
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                      B8215602ACE7AD1F CRC64;
                                                                                                                                                                                                            100.0%; Score 68; DB 2; Ld 100.0%; Pred. No. 0.0042; ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Natl. Acad. Sci. U.S.A. 91:4234-4238(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-1387 FROM N.A. (ISOFORM 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . Biol. Chem. 269:13929-13935(1994).
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and Drosophila frizzled proteins.";
J. Biol. Chem. 270:4705-4711(1995).
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                                                                                                                                                      1315 AA; 134203 MW;
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Pfam; PF01391; Collagen; 7.
Pfam; PF06482; Endostatin; 1.
ProDom; PD000007; Clg_hellx;
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                                                                                               1200 VPIVNLKDEVLSPS 1213
                                                                                                                                                                                                                                                                                                                                            1 VPIVNLKDEVLSPS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genomics 32:436-446(1996).
                                                                                                                                                                                                                                               Local Similarity 100.
nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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                                                                                                                            Collagen.
                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                  Query Match
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SO KW DR
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isp-sib.ch).
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Comment=2 isoforms, 1 (shown here) and 3, are produced by use of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHARACTERIZATION OF ENDOSTATIN, AND PARTIAL SEQUENCE.
MEDLINE=97160848; Pubmed=9008168; DOI=10.1016/S0092-8674(00)81848-6;
O'Really M.S., Boehm T., Shing Y., Pukai N., Vasios G., Lane W.S.,
Flynn E., Birkhead J.R., Olsen B.R., Folkman J.;
"Endostatin: an endogenous inhibitor of angiogenesis and tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF ENDOSTATIN,
MEDLINE=99169382; Pubmed=9501087; DOI=10.1093/emboj/17.6.1656;
Hohenester E., Sasaki T., Olsen B.R., Timpl R.;
Crystal structure of the anglogenesis inhibitor endostatin at 1.5-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i. FUNCTION: Endostatin potently inhibits endothelial cell proliferation and angiogenesis. May inhibit angiogenesis by binding to the heparan sulfate proteoglycans involved in growth factor signaling.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.
-!- SIMILARITY: Contains 1 frizzled (FZ) domain.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                                                                                                                                         SEQUENCE OF 1591-1774 FROM N.A.

MEDLINE=21217748; PubMed=11321448;
Jia S., Zhu F., Li H., He F., Xiu R.-J.;

"Anticancer treatment of endostatin gene therapy by targeting tumor neovasculature in C57/BL mice.";

Clin. Hemorheol. Microcirc. 23:251-257(2000).
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Isold=P39061-1; Sequence=VSP 000303;
Note=Produced by alternative splicing of isoform 1;
Name=3; Synonyms=Short, NC1-301;
Isold=P39061-2; Sequence=VSP 001157, VSP 001158;
TISSUS SPECIFITY: Expressed in liver, kidney, lung, skeletal
muscle and testis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alternative promoters;
Bvente-Alternative splicing; Named isoforms=3;
Name=1; Synonyms=NC1-764;
Isoid=P39061-3; Sequence=Displayed;
proteing.";
Proc. Natl. Acad. Sci. U.S.A. 91:4229-4233(1994)
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AAC52901.1; JOINED.
AAC52901.1; JOINED.
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EMBO J. 17:1656-1664(1998).
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U34613;
U03716;
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AAC52902.1;

Gaps

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[1] -
SEQUENCE FROM N.A.
MEDLINE=21409408; PubMed=11517600;
Feng Y., Cui L.B., Liu C.X., Ma Q.J.;
Find Yi, Cui betect in vitro of purified endostatin expressed in Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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100.0%; Score 68; DB 1; Length 1774; 100.0%; Pred. No. 0.0059; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 86.8%; Score 59; DB 2; Length 187; Best Local Similarity 85.7%; Pred. No. 0.022; Matches 12; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (2)
SEQUENCE FROM N.A.
FOUR Y., WU Y., Zhu X., Liu C.X., Ma Q.J.;
Four Y., WU Y., Zhu X., Liu C.X., Ma Q.J.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF416592; AAL37720.1;
HSSP; P39060; 1BNL.
HSSP; P806482; Endostatin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dou D.;
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF282883; AAM52249.1; -.
HSSP; P39060; 1BML.
InterPro; IPR010515; Endostatin.
InterPro; IPR000001; Kringle.
Pfam; PF06482; Endostatin; 1.
ProDom; PD000395; Kringle; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Collagen.
NON TER 1 1
SEQUENCE 187 AA; 20448 MW; 72B1047D85838CD3 CRC64;
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                                                                                                                                                                                                                            QBWXIS PRELIMINARY; PRT; 187 AA.
01-MAR.5;
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last senotation update)
Collagan XVIII (Fragment).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OMR-2004 (TrEMBLrel. 26, Last annotation update)
Mylti-functional protein MFP.
Homo sapiens (Human)
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Sheng Wu Gong Cheng Xue Bao 17:278-282(2001)
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                                                                                                          1659 VPIVNLKDEVLSPS 1672
                                                                                1 VPIVNLKDEVLSPS 14
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                   Best Local Similarity 100.
Matches 14; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE
  Query Match
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                                                                                                                                                                                  RESULT 9
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BRMBL; U11635; AAC52178.1; -.

BR EMBL; U11635; AAC52178.1; -.

BR EMBL; L22545; AAAC52179.1; -.

BR EMBL; L22545; AAAC5009.1; -.

BR EMBL; L22545; AAAC5009.1; -.

BR PTR; A55101; A55101.

BR PDB; 1DY0; X-ray; A=1340-1527.

BR PDB; 1DX1; X-ray; A=1340-1527.

BR PDB; 1DX1; X-ray; A=1340-1527.

BR GO; GO:0001525; P:angiogenesis; IMP.

BR InterPro; IPR008166; Collagen.

BR InterPro; IPR008166; Collagen.

BR InterPro; IPR0010363; D107959.

BR InterPro; IPR001329; TSP_N.

BR PEam; PP01321; Laminin_G.

BR InterPro; IPR01329; TSP_N.

BR PEam; PP01321; Endostatin; 1.

BR PEam; PP01321; PZ; IN.

BR PEam; PP01321; PZ; IN.

BR PEam; PP01321; PZ; IN.

BR PEAM; SM000210; TSP_N; 1.

BR PEAM; SM00210; FRI; 1.

BRART; SM00210; FRI; 1.

BRART; SM00210; TSP_N; 1.
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Nonhelical region 1 (CCL1).

Triple-helical region 2 (NC2).

Triple-helical region 3 (NC2).

Triple-helical region 3 (NC3).

Triple-helical region 3 (CCL2).

Nonhelical region 4 (NC4).

Triple-helical region 4 (CCL4).

Nonhelical region 5 (NC5).

Triple-helical region 6 (NC5).

Triple-helical region 6 (NC5).

Nonhelical region 6 (NC5).

Nonhelical region 6 (NC5).

Nonhelical region 7 (NC7).
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Nonhelical region 8 (NC8).
Triple-helical region 8 (COL8).
Nonhelical region 9 (NC9).
Triple-helical region 9 (COL9).
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Collagen alpha 1(XVIII) chain.
Endostatin.
TSP N-terminal.
                                                      L, 103716; AACS2902.1; JOINED.
L, 103716; AACS2902.1; JOINED.
L, 103716; AACS2902.1; JOINED.
L, 103716; AACS2903.1; -
L, 103716; AACS2903.1; JOINED.
L, 103716; AACS2903.1; JOINED.
L, 1034609; AACS2903.1; JOINED.
L, 1034609; AACS2903.1; JOINED.
L, 1034610; AACS2903.1; JOINED.
L, 1034611; AACS2903.1; JOINED.
L, 1034613; AACS2903.1; JOINED.
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SIGNAL
1 2
CHAIN 27 177
CHAIN 1591 177
CHAIN 245 43
DOMAIN 365 48
EMBL;
EMBL;
EMBL;
EMBL;
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EMBL;
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Gaps

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1 VPIVNLKDEVLSPS 14
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                                                                                                                                                                                                                                                                           Collagen.
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Matches
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                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to collagen, type XVIII, alpha 1 (Fragment).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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    Length 261;
                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUE=Kidney;
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033715; AAH33715.1; -.
HSSP; P39060; 1BNL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    816 AA; 82553 MW; 5D539B2946694F86 CRC64;
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Last annotation update)
    Score 59; DB 2;
Pred. No. 0.032;
                                                                                                                                                                                                                                  816 AA.
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                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008161; Clg helix.
InterPro; IPR008160; Collagen.
InterPro; IPR010515; Endostatin.
Pfam; PF01391; Collagen; 5.
Pfam; PF0482; Endostatin; 1.
                                                                                                                                                                                                                                                                    01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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05-JUL_2004 (TrEMBLrel, 27, Last seq
05-JUL_2004 (TrEMBLrel, 27, Last ann
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EMBL; AY484967; AAR83298.1; JOINED.
EMBL; AY484969; AAR83298.1; JOINED.
EMBL; AY484970; AAR83298.1; JOINED.
EMBL; AY484971; AAR83298.1;
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    86.8%;
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Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                               147 VPIVNLKDELLFPS 160
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                                                                                     1 VPIVNLKDEVLSPS 14
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Query Match
Best Local Similarity 85.7°
Matches 12; Conservative
                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
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NON TER
SEQÜENCE
                                                                                                                                                                                                                                                   Q8N4S4;
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Q8N4S4
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MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
MEDLINE=20289799; PubMed=10830953; DOI=10.1038/35012518;
MACTORIM, Rujfyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
A. Schartal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
A. Schaff M., Schoen O., Desario A., Reichelt J., Kauer G., Blocker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
Lehrach H., Reinhardt R., Yaspo M.-L.;
When sequence of human chromosome 21.";
Nature 405:311-319(2000).
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MEDLINE=98164096; PubMed=9503365; DOI=10.1016/S0945-053X(98)90003-8;
Saarela J., Ylkarppa R., Rehn M., Purmonen S., Pihlajaniemi T.;
"Complete primary structure of two variant forms of human type XVIII
collagen and tissue-specific differences in the expression of the
corresponding transcripts.";
Matrix Biol. 16:319-328(1998).
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[4]
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MEDILINE-94245237; PubMed-8188291;
Oh S.P., Warman M.L., Seldin M.F., Cheng S., Knoll J.H., Timmons S.,
Olsen B.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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P39060; Q9UK38; Q9Y6Q7; Q9Y6Q8;
D1-FRB-1995 (Rel. 31, Created)
29-MAR-2004 (Rel. 41, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(XVIII) chain precursor [Contains: Endostatin]
Name=COL18A1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.8%; Score 59; DB 2; Length 1336;
85.7%; Pred. No. 0.19;
ive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1336 AA; 135522 MW; 1287BFAB2D5034C3 CRC64;
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005198; F:structural molecule activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPRO08161; Collagen.
InterPro; IPRO08160; Collagen.
InterPro; IPRO10515; Endostatin.
InterPro; IPRO10515; Endostatin.
Pfam; PF01312; Collagen; 6.
Pfam; PF01312; Collagen; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                               ProDom; PD000007; Clg_helix; 1.
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PRCPWPWPRRRRLLDVLAPLVLLLGVRAASAEP (in
                                                                                             MIM; 267750; --
O(0) (20:0005881; C:collagen; TAS.
GO; GO:00008282; P:negative regulation of cell proliferation; TAS.
GO; GO:0009887; P:vaganogenesis; TAS.
GO; GO:0007601; P:vaiual perception; TAS.
InterPro; IPR008161; Callagen.
InterPro; IPR008165; Conlagen.
InterPro; IPR008985; Conlagen.
InterPro; IPR008985; Conlagen.
InterPro; IPR009191; Laminin_G.
InterPro; IPR001791; Laminin_G.
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                                                                                                                                                                                                                                                                                                                         Cell adhesion; Collagen;
Hydroxylation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonhelical region 9 (NC9).
Triple-helical region 9 (COL9).
Onhelical region 10 (NC10).
Triple-helical region 10 (COL10).
Nonhelical region 11 (NC11).
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region 8 (COL8).
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Triple-helical region 1 (COL1)
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Collagen alpha 1(XVIII) chain
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P 001155.
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Nonhelical region 3
Triple-helical region 4
Nonhelical region 4
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'FTIG=VAR_018054
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'FTId=VAR_018055.
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By similarity.
Cell attachment
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                                                                                                                                                                                                                                                                 Pfam; PF06482; Endostatin; 1.
Pfam; PF02210; TSP N; 1.
Probom; PD000007; Člg helix; 1.
SMART; SMO0210; TSPN; 1.
3D-structure; Alternative splicing;
Extracellular matrix; Glycoprotein;
                EMBL; L22548; AAA51864.1; -.
EMBL; AF184060; AAF01310.1; ALT_INIT
PDB; 1BNL; X-ray; A/B/C/D=1334-1511.
                                                                                                                                                                                                                                                                                                                                                      Repeat, Signal, Structural protein.
SIGNAL 1 23 Potent
CHAIN 24 1516 Collag
 AL163302; CAB90482.1; -.
                                                       GlycoSuiteDB; P39060; -.
Genew; HGNC:2195; COL18A1.
MIM; 120328; -.
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Pfam; PF06121; DUF959; 1.
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 the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                  VARIANTS LEU-49; ARG-111; ILE-841 AND ARG-886, AND CHARACTERIZATION OF VARIANT ASN-1437.

PubMed=14695535; DOI=10.1002/humu.10284;
Menzel O., Bekkeheien R.C.J., Reymond A., Fukai N., Boye E.,
Kosztolanyi G., Aftimos S., Deutsch S., Scott H.S., Olsen B.R.,
Antonarakis S.E., Gipponi M.;
"Knobloch syndrome: novel mutations in COL18A1, evidence for genetic heterogeneity, and a functionally impaired polymorphism in
                                                                                                                                                                                                                       VARIANTS ILE-841 AND ASN-1437.

MEDIJNE-21518361; PubMed=11666364;
Iughetti P., Suzuki O., Godoi P.H., Alves V.A., Sertie A.L.,
Zorick T., Soares F., Camargo A.A., Moreira E.S., di Loreto C.,
Moreira-Filho C.A., Simpson A., Oliva G., Passos-Bueno M.R.;
A polymorphism in endostatin, an angiogenesis inhibitor, predisposes
for the development of prostatic adenocarcinoma.";
Cancer Res. 61:7375-7378(2001).
                                                                                                          MEDLINE=20400145; PubMed=10942434; DOI=10.1093/hmg/9.13.2051; Sertite A.L., Sossi V., Camargo A.A., Zatz M., Brahe C., Passos-Bueno M.R.; "Collagen XVIII, containing an endogenous inhibitor of angiogenesis and tumor growth, plays a critical role in the maintenance of retinal structure and in neural tube closure."; Hum. Mol. Genet. 9:2051-2058(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhi Yong H., Biao L., Wei-Jie Z., Xiang-Pu W.,
                                                                    Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                INVOLVEMENT IN KNOBLOCH SYNDROME.
SEQUENCE OF 1334-1516 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor signaling.
ALTERNATIVE PRODUCTS:
             :ISSUE=Placenta;
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,n _ (NC4) . ^ (COL4) .

(COL3).

(NC2) (NC3). (COL6).

(NC6).

(COL7)

(COLS).

(NCS).

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(Potential) (Potential)

(Potential) (Potential)

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SEQUENCE FROM N.A.
MEDLINE=22980396; PubMed=14614989; DOI=10.1016/S0945-053X(03)00073-8;
Elamma H., Snellman A., Rehn M., Autio-Harmainen H., Pihlajaniemi T.;
"Characterization of the human type XVIII collagen gene and
prorecolytic processing and tissue location of the variant containing frizzled motif:";
                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                    | Matrix Biol. 21:477-442 (2003).
| Ratizated motori: ";
| Matrix Biol. 21:427-442 (2003).
| Rambi, AY484968; AAR83296.1; JOINED.
| EMBL; AY484970; AAR83296.1; JOINED.
| Rambi, AY484971; AAR83296.1; JEA.
| GO; GO:000198; F:structural molecule activity; IEA.
| GO; GO:000198; F:structural molecule activity; IEA.
| GO; GO:0007155; P:call adhesion; IEA.
| GO; GO:0007275; P:call adhesion; IEA.
| GO; GO:0007275; P:call adhesion; IEA.
| GO; GO:0007275; P:call adhesion; IEA.
| RitherPro; IPR008161; Clg helix.
| R InterPro; IPR008161; Clg helix.
| R InterPro; IPR010515; Endostatin.
| R InterPro; IPR010515; Endostatin.
| R InterPro; IPR03129; TSP.N.
| R Pfam; PF06131; OUF959: 1.
| R Pfam; PF06132; Endostatin; 1.
| R Pfam; PF06132; Endostatin; 1.
| R Pfam; PF001302; Clg helix; 1.
| R Pfam; PF001302; Clg helix; 1.
   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type XVIII collagen long variant.
Homo sapiens (Human).
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Collagen.
SEQUENCE 1751 AA; 177
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SMART; SM00210; TSPN; 1.
                                                                                                                   NCBI_TaxID=9606;
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                                                                 heterozygotes may cause Knobloch syndrome when in combination with a frameshift/truncating mutation)
/FIId=VAR_012709.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22900396; PubMed=14614989; DOI=10.1016/S0945-053X(03)00073-8;
Blamaa H., Snellman A., Rehn M., Autio-Harmainen H., Pihlajaniemi T.;
"Characterization of the human type XVIII collagen gene and
proteolytic processing and tissue location of the variant containing efrizzled motif.";
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/FTId=VAR 018056.
D -> N (decreased activity for binding laminin; increased risk of developing prostate cancer; in compound
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                             Score 59; DB 1; Length 1516; Pred. No. 0:22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 1516;
                                                                                                                                                                             1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1516 AA; 153779 MW; 38D0F23D3FD758A4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALLINE BIOLITY

MALLINE BIOLITY

MALLINE BIOLITY

EMBL; AV484968; AAR83297.1; JOINED.

EMBL; AV484970; AAR83297.1; JOINED.

EMBL; AV484970; AAR83297.1; JOINED.

EMBL; AV484971; AAR83297.1; JOINED.

GO; GO:0005189; F: Structural molecule activity; IEA.

GO; GO:0005185; F: Structural molecule activity; IEA.

GO; GO:0006185; F: Structural molecule activity; IEA.

GO; GO:0006817; P: P: Posphate transport; IEA.

InterPro; IPR008161; Collagen.

InterPro; IPR010515; Endostatin.

InterPro; IPR003129; TSP N.

Pfam; PP61391; Collagen; 6.
                                                                                                                                                                                                                                                                                                                                                   05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type XVIII collagen middle variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 59; DB 2;
Pred. No. 0.22;
1; Mismatches
                                                                                                                                                                                                                                                                                                                        PRT; 1516 AA.
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Probom; PD000007; Clg helix; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF06121; DUF959; 1.
Pfam; PF06482; Endostatin; 1.
                                                                                                                                             86.8%;
                                                                                                                                                                                                                               1402 VPIVNLKDELLFPS 1415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
                                                                                                                                                                                                           1 VPIVNLKDEVLSPS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 VPIVNLKDEVLSPS 14
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00210; TSPN;
                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
                                                                                                                                                           Local Similarity
nes 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collagen.
SEQUENCE
                                                                                                                                             Query Match
                  VARIANT
                                                                                                                                                                                                                                                                                                                                       26RZ39;
                                                                                                                                                                                                                                                                                                                        Q6RZ39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
Q6RZ40
                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gallus gallus (Chicken).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
Gallus.
NCBL TaxID=9031;
                                                                                                                 Gaps
                                                                                                                 ö
                                              Score 59; DB 2; Length 1751;
Pred. No. 0.26;
1; Mismatches 1; Indels
1751 AA; 177920 MW; 481F4F72176FA2A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                PRT; 1344 AA.
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PRT; 1751 AA.

PRELIMINARY;

Q6RZ40 Q6RZ40;

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RN [2]
RA SEQUENCE FROM N.A.
RA Halfter W., Dong S.;
R. Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

R. Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

B. Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

B. Spi P39060; 1BNL.

CG): GG:0005198; F:structural molecule activity; IEA.

B. GG; GG:0007155; P:cell adhesion; IEA.

CG): GG:0007155; P:cell adhesion; IEA.

B. InterPro; IPR008164; CJg helix.

B. InterPro; IPR008165; Collagen; Gollagen; Gollagen; B.

B. InterPro; IPR001515; Endostatin.

B. InterPro; IPR001515; Endostatin.

B. InterPro; IPR001515; Endostatin.

B. InterPro; IPR001791; Laminin_G.

B. InterPro; IPR001791; IPR001791; IPR001791;

B. InterPro; IP
```

Search completed: March 10, 2005, 11:09:31 Job time : 57.3684 secs

1 VPIVNLKDEVL 11 ||||||:|||| 1229 VPIVNLRDEVL 1239

8 8

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
```

OM protein - protein search, using sw model

March 10, 2005, 11:00:49; Search time 12.1579 Seconds Run on:

(without alignments)
110.795 Million cell updates/sec

1 VPIVNLKDEVLSPS 14 US-09-766-412-31 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:* Database :

pir1:* pir2:* pir3:* 2 K 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Length	DB	αı	Description
1		100.0	1315	2	A56101	collagen alpha 1(X
7	68	100.0	1774	~	B56101	collagen alpha 1(X
e	59	86.8	684	~	A53019	collagen alpha 1(X
4	43	63.2	327	7	T33540	.cal pr
ς,	40	58.8	399	7	T01387	oxidoreductase hom
9	40	58.8	548	7	JC6174	immunodominant 120
7	40		1388	7	A53317	collagen alpha 1(X
œ	39	57.4	187	7	E90390	hypothetical prote
0	39	57.4	264	7	D71724	
10	39	57.4	266	7	A97723	
11	39	57.4	887	7	S41543	DÑA topoisomerase
12	38	55.9	334	7	T04198	hypothetical prote
13	38	55.9	485	7	E88114	protein F53C3.9 [i
14	38	55.9	535	~	S68446	origin recognition
15		'n.	565	7	H82516	60kDa inner-membra
16		55.9	813	Н	D70176	endopeptidase La (
17		55.9	1016	7	T25433	hypothetical prote
18	m	55.9	1222	7	S40977	
19	37.5	. 55.1	425	7	H83652	seryl-tRNA synthet
20		54.4	107	7	AF1948	
21	37	54.4	170	N	T15452	
22		54.4	_	N	F70410	
23	37	54.4	261	~	G69134	hypothetical prote
24	37	54.4		~	H85214	-H
25	37	54.4		~	873159	hypothetical prote
26	37	54.4		~	T20947	hypothetical prote
27	37	54.4	364	7	A89004	T24A
28	37	54.4	404	~	S42831	
29	37	54.4	441	0	T11715	

acetylornithine tr	conserved hypothet	hypothetical prote	hypothetical prote	serine-tRNA ligase .	hypothetical prote	hypothetical prote	elongation factor	tranglation elonga	hypothetical prote	hypothetical prote	serine/threonine-p	CbhB protein - Cox	probable aminotran	hypothetical prote	two-component sens
T42091	T39840	T16368	T15191	S66043	A95121	F97990	H97920	D95050	E75150	G64387	G75345	JQ1189	AB0077	C64401	AE1942
~	~	~	N	~	7	~	~	~	N	٦	~	~	~	(1)	7
442	268	759	1043	425	93	93	186	186	194	226	251	341	410	439	468
54.4	54.4	54.4	54.4	53.7	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9
37	37	37	37	36.5	36	36	36	36	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

tissı

Proc. Natl. Acad. Sci. U.S.A. 91, 4234-4238, 1994 A;Title: Alphal(XVIII), a collagen chain with frequent interruptions in the collagenous A;Reference number: A58371; MUID:94240112; PMID:8183894 1842

Apacession: A58371

AjMolecule type: mRNA
Ajkesierence number: A58371

AjMolecule type: mRNA
Ajkesidues: 1-928 cREH7Ajkesidues: 28-687, 'L', 689-734, 'F', 736-751, 'R', 753-1315 cOHM>
Ajkesidues: 28-687, 'L', 689-734, 'F', 718-751, 'R', 753-1315 cOHM>
Ajkesidues: 28-687, 'L', 689-734, 'F', 718-751, 'R', 753-1315 cOHM>
Ajkesidues: 28-687, 'L', Muragaki, 'Y', Timmons, S.; Ooshima, A.; Olsen, A.B.R.
R'Ob, S.P.; Kamagata, 'Y.; Muragaki, 'Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl.
Ajkesidues: 28-687, 'L', Muragaki, 'Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Proc. Natl.
Ajkesidues: 28-887, 'Muragata, 'Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.
Ajtite: Isolation and sequencing of conna for proteins with multiple domains of Gly-Xa
Ajtite: Isolation and sequencing of conna for proteins with multiple domains of Gly-Xa
Ajkesidues: 28-1315 cOHMA
Ajkesidues: 28-1315

C, Genetics

A,Cross-references: MGI:71175
A;Map position: 10:41.0
C;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly.
C;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly.
F;1-25/Domain: signal sequence #status predicted <SIG>
F;24-225/Region: thrombospondin amino-terminal homologous
F;26-1315/Product: collagen alpha 1(XVIII) chain, short splice form #status predicted <

E.; Bi

```
A, Molecule type: protein
A, Residues: 1591-1610 < ORB>
A, Residues: 1591-1610 < ORB>
A, Experimental source: hemangioendothelium cells
A, Note: inhibite endothelial cell proliferation
C, Comment: Prolines and lysines at the third position of the tripeptide repeating unit lated and subsequently O-glycosylated.
C, Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in periC, Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of un ay be useful in treating solid tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 10:41.0

A;Introns: 1295/3; 1311/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1599,
A;Introns: 1295/3; 1310/1; 1331/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1599,
A;Note: the list of introns is incomplete
C;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly:
F;1-1374/Product: collagen alpha 1(XVIII) chain precursor, long splice form #status pred;
F;1-24/Domain: signal sequence #status predicted <SIG>F;786-812/Domain: collagenous #status predicted <CO01>F;823-896/Domain: collagenous #status predicted <CO02>F;823-896/Domain: collagenous #status predicted <CO03>F;823-896/Domain: collagenous #status predicted <CO03-F;823-896/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C,Accession: A53019
R;Oh, S.P.; Warman, W.L.; Seldin, M.F.; Cheng, S.D.; Knoll, J.H.M.; Timmons, S.; Olsen, Bennics 19, 494-499, 1994
A;Title: Cloning of cDNA and genomic DNA encoding human type XVIII collagen and localiz. A;Reference number: A53019; MUID:94245237; PMID:8188291
A, Title: Primary structure of the alphal chain of mouse type XVIII collagen, partial sti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig. 1066-1148/Domain: collagenous #status predicted <CCO5-
Filose-1204/Domain: collagenous #status predicted <CCO5-
Filose-1204/Domain: collagenous #status predicted <CCO5-
Filose-1304/Domain: collagenous #status predicted <CCO6-
Filose-1304/Domain: collagenous #status predicted <CCO6-
Filose-1304/Domain: collagenous #status predicted <CCO6-
Filose-1354/Region: cell attachment (R-G-D) motif
Filose-1704/Product: collagenous #status predicted <CCO6-
Filose-1704/Product: endostatin #status predicted <CCO6-
Filose-1704/Product: endostatin #status predicted <EST>
Filose-1704/Product: end
                                                                                                                                                                                                                                                                                       A;Residues: 1293-1403, "R',1405-1774 <REH3>
A;Cross-references: GB:U03714; NID:g487733; PIDN:AAA20657.1; PID:g487734
R;O'Reilly, M.S.; Boehm, T.; Shing, Y.; Fukai, N.; Vasios, G.; Lane, W.S.; Flynn, Cell 89, 277-285; 1997
A;Title: Endostatin: an endogenous inhibitor of angiogenesis and tumor growth.
A;Reference number: A58816; MUID:97160848; PMID:9008168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(XVIII) chain - human (fragment)
N;Contains: endostatin
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #Beguence_revision 18-Aug-1995 #text_change 15-Sep-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-684 cOHA-
A;Cross-references: GB:L22548; NID:9348908; PIDN:AAA51864.1; PID:9562794
A;Cross-references: GB:L22548; NID:9348908; Is not in Genbank release 103
A;Note: the cited accession number, L25548, is not in Genbank release 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 68; DB 2; Length 1774; 100.0%; Pred. No. 0.0011; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;921-1042/Domain: collagenous #status predicted <CO03>
                                                                                                                                     A; Reference number: A54072; MUID: 94245707; PMID: 8188673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1659 VPIVNLKDEVLSPS 1672
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: MGI:Coll8a1
A;Cross-references: MGI:71175
                                                                                                                                                                                                                                                                   A; Molecule type: DNA; mRNA A; Residues: 1293-1403, 'R', '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: A58816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A53019
                                                                                             collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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C. Date: 0.0 -005-1938 Laptance revision 08-May-1998 Hear_change 09-Unl-2004
C. Date: 0.0 -005-1938 Heagtence revision 08-May-1998 Hear_change 09-Unl-2004
C. Date: 0.0 -005-1938 Heagtence revision 08-May-1998 Hear_change 09-Unl-2004
C. Date: 0.0 -005-1938 Heagtence revision 06-May-1998 Hear_change 09-Unl-2004
C. Date: 0.0 -005-1938 Heagtence revision of three Nucleminal ends of type XVIII collagen chains and tissu tif homologous to rate and Drosephia firized proteins
A. Accession: B65.01
A. Molecule type: MRNA
A. Residues: 1-233, 487-562 RRH3
A. Accession: C56.01
A. Molecule type: MRNA
A. Residues: 1-234, 487-562 RRH3
A. Accession: C56.01
A. Molecule type: MRNA
A. Mole
F;327-353/Domain: collagenous #status predicted <CO2>
F;364-37/Domain: collagenous #status predicted <CO2>
F;466-583/Domain: collagenous #status predicted <CO3>
F;607-689/Domain: collagenous #status predicted <CO3>
F;607-689/Domain: collagenous #status predicted <CO3>
F;704-745/Domain: collagenous #status predicted <CO5>
F;798-811/Domain: collagenous #status predicted <CO6>
F;842-814/Domain: collagenous #status predicted <CO6>
F;887-910/Domain: collagenous #status predicted <CO6>
F;887-910/Domain: collagenous #status predicted <CO6>
F;887-910/Domain: collagenous #status predicted <CO8>
F;982-1315/Product: endostatin #status predicted <CO9>
F;132-1315/Product: endostatin #status predicted <EST>
F;1132-1315/Product: endostatin #status predicted <EST>
F;1132-1315/Product: endostatin #status predicted <EST>
F;1132-1315/Region: multiplexin collagen carbobxyl-terminal homologous F;126,488/Binding site: carbohydrate (Asn) (covalent) #status predicted F;240,245,1257/Binding site: carbohydrate (Ser) (covalent) #status predicted F;451,454,594/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               collagen alpha 1(XVIII) chain precursor, long splice form - mouse N;Contains: collagen alpha 1(XVIII) chain precursor, medium splice form; endostatin C;Species: Mus musculus (house mouse) C;pacies: Mus musculus (house mouse) C;pacies: O3-Oct-1995 #sequence_revision 08-May-1998 #text change 09-Jul-2004 C;Accession: B56101; C56101; S72450; S65595; PN0675; A54072; A58816 R;Rehn, M.; Pihlajaniemi, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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nes 14; Conservative (
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Gaps

us-09-766-412-31.rpr

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Gape

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C;Accession: JC6174
R;Yu, X.; Crocquet-Valdes, P.; Walker, D.H.
Gene 184, 149-154, 1997
A;Title: Cloning and sequencing of the gene for a 120-kDa immunodominant protein of Ehr
A;Reference number: JC6174; MUID:97183655; PMID:9031621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1.548 < YUA>
A; Residues: 1.548 < YUA>
A; Cross-references: UNIPROT: Q46976; GB: U49426; NID: g1864025; PIDN: AAC44861.1; PID: g1864: C; Comment: This protein is an immunodominant antigen of Ehrlichia chaffeensis which reachtogenicity of Ehrlichia chaffeensis and stimulating protective immunity in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Notation at pina 1(XV) chain precursor - human
Nighternate names is procollagen alpha 1(XV) chain
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 09-Jul-2004
C;Accession: A5317, A5146; S28778
R;Kivitrikko, S.; Heinaemaeki, P.; Rehn, M.; Honkanen, N.; Myers, J.C.; Pihlajaniemi, T.
J; Biol. Chem. 269, 4773-4779, 1994
A;Title: Primary structure of the alphal chain of human type XV collagen and exon-intro-A;Reference number: A53317; MUID:94148920; PMID:8106446
A;Accession: A53317
A;Accession: A53317
A;Molacuit et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule Lype: mRNA

A; Residues: 1-1388 <KIV.>
A; Residues: 1-1388 <KIV.>
A; Cross-references: UNIPROT: P39059; GB:L25280
A; Note: nucleotide sequence and conceptual translation not complete
A; Note: nucleotide sequence and conceptual translation at Complete
A; Muragaki, Y:, Abe, N:, Ninomy, Y:, Olsen, B.R.; Ooshima, A.
J: Biol. Chem. 269, 4042-4046, 1994
A; Title: The human alpha!(XV) collagen chain contains a large amino-terminal non-triple
A; Reference number: A53146; MUID:94140817; PMID:8307960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: A53146
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-9,'S',11-48,'V',50-94,'A',96-149,'A',151-203,'V',205-408,'A',410-569 <MUR
A;Cross-references: GB:D21230; NID:g415605; PIDN:BAA04762.1; PID:d1005294; PID:g460703
                                                 A,Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-399 <PAR>
A;Residues: 1-399 <PAR>
A;Cross-references: UNIPROT:Q9ZTA2; EMBL:AF069442; NID:g3242970; PID:g3924598
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunodominant 120K protein - Bhrlichia chaffeensis
C;Species: Bhrlichia chaffeensis
C;Date: 11-Apr-1997 #sequence_revision 09-May-1997 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2;
Pred. No. 37;
                                                                                                                                                                                                                                                                                    A,Introns: 123/2; 167/3; 313/3
A;Note: T419.6
C;Superfamily: 1-aminocyclopropane-1-carboxylate
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40; DB 2
Pred. No. 25;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                              58.8%;
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LPLINLADKTLEP 20
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Best Local Similarity 50...
Retroat 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JC6174
A; Molecule type: DNA
                     A; Accession: T01387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein F58E1.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T33540
R;Wammaley, P.; Twyman, B.
submitted to the EMBL Data Library, October 1998
A;Description: The sequence of C. elegans cosmid F58E1.
A;Reference number: 221365
A;Accession: T33540
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-327 *WAM>
A;Residues: 1-327 *WAM>
A;Coss-references: UNIPROT:Q9TZF8; EMBL:AF098995; PIDN:AAC67479.1; GSPDB:GN00020; CESP:A;Coss-references: Etrain Bristol N2; clone F58E1
C;Genetics:
A;Genetics:
A;Genetics:
A;Mapposition: 2
A;Mapposition: 2
A;Mapposition: 2
A;Note: in the authors' translation, 482-Gly is not shown, residues 483-490 are shifted C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (lated and subsequently O-Glycosylated.
C;Comment: Different splice forms of collagen alpha 1(XVIII) may be involved in perivase C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of unity be useful in treating solid tumors.
                                                                                                                                                                                                                                                                                A;Cross-references: GDB:138752; OMIM:120328
A;Map position: 21q22.3 -21q22.3
A;Map position: 21q22.3-21q22.3
C;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteoglyc
C;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteoglyc
F;1-684/Product: collagen alpha 1(XVIII) chain (fragment) #status predicted <CO4>
F;1-597/Omain: collagenous #status predicted <CO5>
F;129-201/Domain: collagenous #status predicted <CO5>
F;212-244/Domain: collagenous #status predicted <CO5>
F;222-244/Domain: collagenous #status predicted <CO5>
F;222-248/Domain: collagenous #status predicted <CO5>
F;222-248/Domain: collagenous #status predicted <CO6>
F;252-2284/Region: cell attachment (R-G-D) motif
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CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiDate: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
CiAccession: T01387
RiParnell, L.D.; Gnoj, L.; de la Bastide, M.; Hameed, A.; Habermann, K.; Schutz, K.; Hua submitted to the EMBL Data Library, May 1998
A;Description: Genomic sequence of BAC T419 from Arabidopsis thaliana, chromosome IV, ne A;Reference number: Z14314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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Pred. No. 5.6;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 684;
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Pred. No. 0.016;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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85.7%;
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Best Local Similarity 64.3%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        570 VPIVNLKDELLFPS 583
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Best Local Similarity 85.7
Matches 12; Conservative
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                                                                                                                                                                                                                       Genetics:
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A; MCGCULE type: DNA
A; Residues: 1-784, S', 786, C', 788-887 <FOW>
A; Residues: 1-794, S', 786, C', 788-887 <FOW>
A; Cross-references: EMBL:M97227, NID:9478995; PIDN:AAA22859.1; PID:9478996
A; Experimental source: strain 7702
B; Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle
B; Okinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, P.; Koehle
A; Bacteriol. 181, 6509-6515, 1999
A; Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbor
A; Reference number: A59091; MUID:99445483; PMID:10515943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Cross-references: UNIPROT: 092J84; GB: AE006914; PIDN: AAL02723.1; PID: 915619234; GSPDB: C, Genetics:
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R;Fouct, A.; Sirard, J.C.; Mock, M.
submitted to the EMBL Data Library, May 1994
A;Description: Bacillus anthracis pXO1 virulence plasmid encodes a type 1 DNA topoisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-84, S',786,'C',788-887 <OKI>
A;Cross-references: GB:APO65404; NID:g4894216; PIDN:AAD32445.1; PID:g4894357
A;Experimental source: strain Sterne
A;Experimental source: strain Sterne
A;Note: similar to type 1 DNA topoisomerase, top1, plasmid pXO1; B. anthracis (M97227)
C;Genetics:
A;Gene: topX; pXO1-142
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C;Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S41543; S78064; E59108
R;Fouet, A.; Sirard, J.C.; Mock, M.
Mol. Microbiol. 11, 471-479; J94
A;Title: Bacillus anthracis pXO1 virulence plasmid encodes a type 1 DNA topoisomerase.
A;Reference number: S41543; MUID:94203050; PMID:8152371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cjaccesion: A97723
R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.B.; Barbe, V.; Samson, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Rickettsia conoril and Rickettsia prowazekii. AjReference number: A97700; MUID:21442074; PMID:11557893
                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein RC0185 [imported] - Rickettsia conorii (strain Malish 7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C, Species: Rickettsia conorii
C, Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          topoisomerase (EC 5.99.1.2) - Bacillus anthracis virulence plasmid pXO1
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       Length 264;
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           5
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       Score 39; DB 2
Pred. No. 23;
3; Mismatches
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24:
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Pred. No.
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A,Residues: 1-887 <FOU>
A,Cross-references: UNIPROT:P40114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57.4%;
           57.48;
                                               63.68;
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                                                                                      7; Conservative
                                                                                                                                                                                                                                         152
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                                                                                                                                                                 4 VNLKDEVLSPS 14
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                                                                                                                                                                                                         |: |||::|||
142 VDSKDEIISPS
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Matches 7; Conserv
           Query Match
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S41543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Accession: A97723
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submitted to GenBank, April 2001
A; Description: Sulfolobus solfataricus complete genome.
A; Reference number: A99139
A; Accession: E90390
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-167 < KOR.
A; Residues: 1-167 < KOR.
C; Genetics:
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R;Andersson. Borguence_revision 21-Nov-1998 #text_change 09-Jul-2004
C;Accession: D71724
R;Andersson. S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, U
Nature 396, 133-140, 1998
A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A;Reference number: A71630; MuID:99039499; PMID:9823893
A;Accession: D71724
A;Scatus: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-264 cAND>
A;Cross-references: UNIPROT:Q9ZE19; GB:AJ235270; GB:AJ235269; NID:g3860572; PIDN:CAA1461
A;Experimental source: strain Madrid E
A;Gene: RP143
R;Myers, J.C.; Kivirikko, S.; Gordon, M.K.; Dion, A.S.; Pihlajaniemi, T.
Proc. Natl. Acad. Sci. U.S.A. 89, 10144-10148, 1992
A;Title: Identification of a previously unknown human collagen chain, alphal(XV), charac A;Fitle: Identification of a previously unknown human collagen chain, alphal(XV), charac A;Reference number: S28778; MUID:93066196; PMID:1279671
A;Recession: S28778
A;Residues: preliminary
A;Residues: B44-640, P', 642-811, 'P', 813-1252 <MYE>
C;Genetics:
A;Genetics:
A;Gen
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Species: Rickettsia prowazekii
Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein SSO2210 [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 15;
3; Mismatches
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1273 LPIVNLKGQVL 1283
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Matches 8, Conservative
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56 PIYDLKDDILS 66
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A, Gene: SSO2210
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A;Molecule type: DNA
A;Residues: 1-535 <LEA>
A;Cross-references: UNIPROT:Q09142; EMBL:U38472; NID:g1185460; PIDN:AAC49165.1; PID:g11
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, March 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Datession: H82316
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seque.
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
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A;Status: preliminary
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-565 <SIM>
A;Cross-references: UNIPROT:Q9P9U1; GB:AE004083; GB:AE003849; NID:g9108022; PIDN:AAF855
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinard, E.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; R; Briones, M.R.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, Sas-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
sa-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
sa-Neto, E.; Docena, C.; El-Dorry, H.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frob, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laig chado, M.A.; Madeira, A.M. B.N.; Madeira, H.M.F.; Matsukuma, A.Y.; Menck, C.L.; Marquee, M.V.; Mattins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.W.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunse, L.R.; Oliveara, M.A.; de Oliveara, M.C.; de Oliveara, R.C.; Palmieri, D.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G; Santelli, R.V.; Sawasa, A; Authors da Silva, A.C.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A.M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: probable 60K inner membrane protein; stage III sporulation protein homol
   recognition complex protein, subunit 2 - fission yeast (Schizosaccharomyces pomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:AL049474; PIDN:CAB39366.1; GSPDB:GN00067; SPDB:SPBC685.09
A;Experimental source: strain 972h-; cosmid c685
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inner-membrane protein XF2780 [imported] - Xylella fastidiosa (strain 9a5c)
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                             NyAlternate names: replication factor Orp2
C,Species: Schlzosacdnaromyces pombe
C,Species: Schlzosacdnaromyces pombe
C,Accession: S68446; T40640
C;Accession: S68446; T40640
S;Leatherwood, J; Lopez-Girona, A.; Russell, P.
Nature 379, 360-363, 1996
A;Title: Interaction of Cdc2 and Cdc18 with a fission yeast ORC2-like protein.
A;Reference number: S68446; MUID:96149252; PMID:8552194
A;Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Map position: 2
C;Function:
A;Description: interacts with the rate-limiting replication activator Cdc18
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A,Accession: T40640
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,MOJecule type: DNA
A,Residues: 1-535 <SEE>
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Pred. No. 83;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Keywords: DNA replication; nucleus
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Best Local Similarity 57.1%;
Matches 8; Conservative
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112 VPLYSLEAEPLSPS 125
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: To.May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: B8B114
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-485 <STO>
A;Coss-references: UNIPROT:09TXTO; GB:chr_II; PIDN:AC67460.1; PID:93786487; GSPDB:GNOOG C;Genetics:
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Pred. No. 47;
0; Mismatches 4; Indels
                                                                                                Length 887;
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                                                                                                                                                            Indels
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A,Map position: 2
C,Superfamily: Caenorhabditis elegans ZK1236.4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein T4F9.90 - Arabidopsis thaliana
                                                                                             Score 39; DB 2;
Pred. No. 1e+02;
5; Mismatches
A;Genome: plasmid
C;Keywords: DNA binding; isomerase
                                                                                         Query Match 57.4%;
Best Local Similarity 46.2%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 55.9%;
Best Local Similarity 66.7%;
Matches 8; Conservative
                                                                                                                                                                                                                                                            |:: :|:||:||
237 PVMKTEDQVLNPS 249
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                                                                                                                                                                                                                        2 PIVNLKDEVLSPS 14
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S68446
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0; Gaps Query Match 55.9%; Score 38; DB 2; Length 565; Best Local Similarity 54.5%; Pred. No. 88; Matches 6; Conservative 4; Mismatches 1; Indels

0

1 VPIVNLKDEVL 11 ||:|:|:|| 74 VPVINVKTDVL 84

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Search completed: March 10, 2005, 11:10:08 Job time : 13.1579 secs

us-09-766-412-31.rapb

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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.
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March 10, 2005, 11:07:00 ; Search time 85.1053 Seconds (without alignments) 54.260 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-766-412-31 68 1 VPIVNLKDEVLSPS 14 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1396920 segs, 329844858 residues Searched:

1396920 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

| Cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.ppp:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* Published Applications AA:* 111. 112. 113. 114. 116. 119. 119.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 31, Appl	Sequence 46, Appl	Sequence 18, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 2, Appli	Sequence 3, Appli	Sequence 71, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 5, Appli	Sequence 11, Appl
	ID	US-09-766-412-31	US-10-131-241-46	US-10-292-418-18	US-10-920-820-13	US-09-998-831-13	US-10-373-561-13	US-09-373-938-2	US-10-080-797-3	US-10-422-934-71	US-10-468-759-2	US-09-822-540A-1	US-09-978-531-5	US-09-978-531-11
	DB	6	14	14	17	σ	14	σ	13	14	15	0	σ	6
	Query Match Length DB	14	184	184	184	191	191	207	207	207	43	63	63	63
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	86.8	86.8	86.8	86.8
	Score	89	68	68	68	68	68	68	9	68	29	59	59	29
	Result No.	п	7	m	4	S	9	7	80	σ	10	11	12	13

Sequence 12, Appl	Seguence 164, App	Sequence 3, Appli	Sequence 60, Appl	Sequence 5, Appli	Seguence 57, Appl	Sequence 47, Appl	Sequence 56, Appl	Sequence 55, Appl	Sequence 14, Appl	Sequence 54, Appl	Sequence 3, Appli	Sequence 14, Appl	-:	۲,	Sequence 1, Appli	ഹ	4.	Sequence 11, Appl	Sequence 2, Appli	Sequence 12, Appl	Sequence 162, App	Sequence 4, Appli	Sequence 4, Appli	5, A	Sequence 2, Appli	ý	301	S	Sequence 166, App	Sequence 3, Appli	4
US-09-978-531-12	S US-10-210-172-164	US-09-978-531-3	4 US-10-131-241-60	4 US-10-042-347-5	4 US-10-131-241-57	4 US-10-131-241-47	4 US-10-131-241-56	4 US-10-131-241-55	US-09-998-831-14	4 US-10-131-241-54	4 US-10-042-347-3	4 US-10-373-561-14	US-09-873-676-2	US-09-978-531-1	3 US-10-080-797-1			5 US-10-135-872B-11				6 US-10-449-609-4	7 US-10-849-650-4	US-09-373-938-5	US-1	Þ	US-1(US-0	US-10-	5 US-10-431-642-3	0 US-09-938-391-4
139 9	160 1	171 9	-	178 1	7	٦	180 1	181 1,	-	182 1	182 1	182 1	183 9	183 9	183 1	7	7	-	٦	183 1	-	184 1	-	208 9	220 1.	7	-	٦	9	516 1	4
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59	23	59	29	29	29	29	23	29	29	29	29	29	29	29	23	29	29	29	59	29	59	59	29	53	53	23	59	29	59	29	28
14	15	16	17	18	19	20	21	22	23	24	25	26.	27	28	29		31		33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 31, Application US/09766412

Batent No. US2002010312941

GENERAL INFORMATION:
APPLICANT: GE, RUOWEN et al.
TITLE OF INVENTION: SMALL PEPTIDES HAVING ANTI-ANGIOGENIC AND ENDOTHELIAL CELL INHIB
TITLE OF INVENTION: ACTIVITY
TITLE OF INVENTION: ACTIVITY
FILE REPERENCE: 1781-02159
CURRENT APPLICATION NUMBER: US/09/766,412
CURRENT PILING DATE: 2001-01-1
NUMBER OF SEQ ID NOS: 50
SOFTWARE PATENTIN VERSION 3.1
SEQ ID NO 31
LENGTH: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 68; DB 9; Length 14; Best Local Similarity 100.0%; Pred. No. 3.2e-05; Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FEATURE:
NAME/KEY: misc feature
; OTHER INFORMATION: Endo-3
US-09-766-412-31
                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Mammalian
RESULT 1
US-09-766-412-31
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Gaps

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RESULT 2
US-10-131-241-46
Sequence 46, Application US/10131241
Publication No. US20030012792A1
GENERAL INFORMATION:

Gaps

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Sequence 13, Application US/0999831

Fatent No. US20020119153A1

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: INHIBITING VGGF

TITLE OF INVENTION: INHIBITING VGGF

TITLE OF INVENTION: INHIBITING VGGF

CURRENT APPLICATION NUMBER: US/09/998,831

CURRENT APPLICATION NUMBER: US/09/561,108

FRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: AD21802
CURRENT APPLICATION NUMBER: US/10/373,561
CURRENT APPLICATION NUMBER: US/10/373,561
FILE REFERENCE: 2003-02-24
PRIOR APPLICATION NUMBER: US/09/561,499
PRIOR APPLICATION NUMBER: (US/09/561,499
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 1999-04-28
NUMBER: OF SEQ ID NOS: 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-998-831-13
                                                                                                                                                                                                                                                                                                                                     Length 184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 68; DB 9; Length 191; 100.0%; Pred. No. 0.0006; Live 0; Mismatches 0; Indel8
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CURRENT APPLICATION NUMBER: US/10/920,820
CURRENT FILING DATE: 2004-08-17
PRIOR APPLICATION NUMBER: US/09/938,391
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 13
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                          Score 68; DB 17;
Pred. No. 0.00058;
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100.0%;
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            14; Conservative
                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: MURINE
US-10-920-820-13
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                           APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: Compositions Angiogenesis Using Cancer Markers
FILE REPERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR APPLICATION NUMBER: US 60/316,802
PRIOR APPLICATION NUMBER: US 60/316,806
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR PILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 46
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Publication No. US20050009144A1
GENERAL INFORMATION:
APPLICANT: Pfizer, Inc. and Pfizer Products, Inc.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING DISORDERS
FILE OF INVENTION: INVOLVING ANGIOGENESIS
FILE REFERENCE: 3153.00234/PCI0790A
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APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: 05/202-11-2
PRIOR APPLICATION NUMBER: 09/382.5
PRIOR PILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 184
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Pred. No. 0.00058;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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Sequence 18, Application US/10292418
Publication No. US20030139365A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 14; Conservative 0,
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lo, Kin-Ming APPLICANT: Li, Yue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ), ORGANISM: Mus musculus
US-10-292-418-18
                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Murinae sp. US-10-131-241-46
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                                                                                       Sequence 71, Application US/10422934

Publication No. US20030186841A1

GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F., III
APPLICANT: Radan, Michael
APPLICANT: Beerli, Roger
APPLICANT: Roger
TITLE OF INVENTION: LIGAND ACTIVATED TRANSCRIPTIONAL REGULATOR PROTEINS
FILE REFERENCE: 22908-1227C
CURRENT APPLICATION NUMBER: US/10/422,934
CURRENT PILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 09/483,042
PRIOR APPLICATION NUMBER: 09/433,042
PRIOR APPLICATION NUMBER: 09/433,042
PRIOR APPLICATION NUMBER: 09/431,042
SEQ DE NOS: 92
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 71
LENGTH: 207
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Pred. No. 0.0044;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10468759
Publication No. US20040073007A1
GENERAL INFORMATION:
APPLICANT: Universita degli Studi di Milano
TITLE OF INVENTION: Peptides with anglogenic activity
FILE REFERENCE: 683pct
CURRENT APPLICATION UNMBER: US/10/468,759
CURRENT FILING DATE: 2003-08-25
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.1
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Patent No. US20020058620A1
GENERAL INFORMATION:
APPLICANT: Phoenix Pharmaceuticals, Inc.
APPLICANT: Chang, Jaw-Kang
TITLE OF INVENTION: Cell Growth Regulation System
FILE REFERENCE: PhoenixPharFull
CURRENT APPLICATION NUMBER: US/09/822,540A
CURRENT FILING DATE: 2001-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-422-934-71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-822-540A-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/0913938
| Publication No. US20020115202A1 |
| GENERAL INRORMATION: |
| APPLICANT: Hallenbeck, Paul |
| APPLICANT: Chen, Cheavyun Theresa |
| TITLE OF INVERTION: ADENOVIRAL VECTORS INCLUDING DNA SEQUENCES ENCODING ANGIOGENIC IN |
| TITLE OF INVERTION ADENOVIRAL VECTORS INCLUDING DNA SEQUENCES ENCODING ANGIOGENIC IN |
| TITLE OF INVERTION DATE: 1999-08-13 |
| CURRENT APPLICATION NUMBER: US/09/373,938 |
| CURRENT ELING DATE: 1999-08-13 |
| NUMBER OF SEQ ID NOS: 17 |
| SEQ ID NO 2 |
| LENGTH: 207 |
| TYPE: PRT |
| ORGANISM: MUB musculus |
| US-09-373-938-2
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                                                                                                                                                                                                                                       Gaps
                                                                                                                ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-10-373-561-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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                                                                                                                                                                                    Query Match 100.0%; Score 68; DB 14; Length 191; Best Local Similarity 100.0%; Pred. No. 0.0006; Matches 14; Conservative 0; Mismatches 0; Indels (
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; Pred. No. 0.00066;
0; Mismatches 0;
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; Sequence 3, Application US/10080797
; Publication No. US20020183253A1
; GENERAL INFORMATION:
; APPLICANT: Campochiaro, Peter A.
; APPLICANT: Dixon, Katharine H.
; APPLICANT: Brazzell, Romilus K.
; TITLE OF INVENTION: METHOD FOR TREATING OCULAR; TITLE OF INVENTION: METHOD FOR TREATING CURRENT APPLICATION NUMBER: US/10/080,797
; CURRENT APPLICATION NUMBER: US/10/080,797
; UNDMER OF SEQ. ID NOS: 21
; NUMBER OF SEQ. ID NOS: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Best Local Similarity 100.0%;
Matches 14; Conservative 0;
                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92 VPIVNLKDEVLSPS 105
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Best Local Similarity 100.
Matches 14; Conservative
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ORGANISM: Mouse
SEQ ID NO 13
LENGTH: 191
TYPE: PRT
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LENGTH: 207
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                                                                                            FEATURE:
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VS-09-978-531-12

VS-09-978-531-12

Sequence 12, Application US/09978531

Sequence 12, Application US/09978531

Sequence 12, Application VS-08020086007A1

Sequence 12, Application VS-08020086007A1

SEQUENCE INFORMATION:

APPLICANT: Sim, Kim Lee

APPLICANT: Sim, Kim Lee

APPLICANT: Liang, Hong

TITLE OF INVENTION: Anglogenesis-Inhibiting Peptides and Proteins and Methods of Use

FILE REFERENCE: 05213-0811 43170-264992

CURRENT APPLICATION NUMBER: US/09/978,531

CURRENT APPLICATION NUMBER: US 60/240,127

PRIOR FILING DATE: 2000-10-13

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PATENTING TO SEQ ID NOS: 13

SEQ ID NO 12

LENGTH: 139

TYPE: PRT

ORGANISM: Homo sapiens

US-09-978-531-12
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Pred. No. 0.017;
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Publication No. US20040043928A1
GENERAL INFORMATION:
APPLICANT: Kekuda, Ramesh:
APPLICANT: Miller, Charles
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Casman, Stacie
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Alsobrook II, John
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Zerhusen, Bryan
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Rastelli, Luca
Spytek, Kimberly
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MacDougall, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VPIVNLKDEVLSPS 14
                     1 VPIVNLKDEVLSPS 14
                                                           6 VPIVNIKDELLFPS 19
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Voss, Edward
Boldog, Ferenc
Gorman, Linda
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Best Local Similarity 85.7
Matches 12; Conservative
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Vernet, Corine
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Ji, Weizhen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pena, Carol
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US-09-978-531-11
is Sequence 11, Application US/09978531
is Publication No. USZ0020086007A1
is Publication No. USZ0020086007A1
is GENERAL INFORMATION:
is APPLICANT: Sim, Kim Lee
is APPLICANT: Sim, Kim Lee
is APPLICANT: Sim, Kim Lee
is APPLICANT: Liang, Hong
is TILE REFERENCE: 05213-0811 43170-264992
is CURRENT APPLICATION NUMBER: US/09/978,531
is CURRENT APPLICATION NUMBER: US 60/240,127
is PRIOR APPLICATION NUMBER: US 60/240,127
is NUMBER OF SEQ ID NOS: 13
is SOFFWARE: PatentIn version 3.1
is SEQ ID NO 11
is LENGTH: 63
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/09978531
Sequence 5, Application US/09978531
Publication No. US20020086007A1
GENERAL INFORMATION:
APPLICANT: Liang, Hong
TITLE OF INVERTYON: Anglogenesis-Inhibiting Peptides and Proteins and Methods of Use
FILE REFERENCE: 05213-0811 43170-254992
CURRENT APPLICATION NUMBER: US/09/978,531
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 60/240,127
PRIOR PELLING DATE: 2000-10-13
NUMBER OF SEQ ID NOS: 13
SEQ ID NO 5
LENGTH: 63
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Pred. No. 0.0068;
1; Mismatches 1; Indels
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Pred. No. 0.0068;
1; Mismatches 1; Indels
                                                                                                                                                                                                         86.8%; Score 59; DB 9; Length 63;
85.7%; Pred. No. 0.0068;
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PRIOR APPLICATION NUMBER: 60/194,561
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
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85.7%;
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Best Local Similarity 85.7
Matches 12; Conservative
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Best Local Similarity 85.7
Matches 12; Conservative
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Matches 12; Conservative
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CORGANISM: Homo sapiens
US-09-978-531-5
                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-822-540A-1
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US-09-978-531-5
                                                                                                         LENGTH: 63
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CURRENT FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/309,501
PRIOR FILING DATE: 2001-08-02
PRIOR PLILING DATE: 2001-08-02
PRIOR PLILING DATE: 2001-08-02
PRIOR PLILING DATE: 2001-08-03
PRIOR PLILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/311,979
PRIOR PLILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/311,892
PRIOR PLILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR APPLICATION NUMBER: 60/312,892
PRIOR PLING DATE: 2001-08-17
PRIOR PLILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: 60/312,892
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PRIOR APPLICATION NUMBER: 60/312,892
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PRIOR APPLICATION NUMBER: 60/312,892
PRIOR PLING DATE: 2001-08-17
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CURRENT APPLICATION NUMBER: US/10/210,172
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Best Local Similarity 85.7
Matches 12; Conservative
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0; Gaps

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Search completed: March 10, 2005, 11:15:27 Job time : 86.1053 secs

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5, Appli
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                                                                                                March 10, 2005, 11:04:09; Search time 28.3684 Seconds (without alignments) 36.840 Million cell updates/sec
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Sequence 13, 7
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Sequence 13, 7
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd
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US-09-602-787A-298
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US-09-938-391A-13
US-09-561-108-13
US-09-561-526-13
US-09-998-831-13
US-09-998-831-13
US-09-951-499-13
US-09-951-499-13
US-09-155-1005-13
US-09-822-540A-1
US-09-82-540A-1
US-09-561-108-14
US-09-561-108-14
US-09-561-99-14
US-09-561-99-14
US-09-561-05-14
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-09-961-403-5
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Maximum Match 100%
Listing first 45 summaries
                                                                  OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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68
1 VPIVNLKDEVLSPS 14
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Maximum DB seq length: 200000000
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Sequence 31, Application US/09385442

Sequence 31, Application US/09385442

Sequence 31, Application US/09385442

Sequence 31, Application US/09385442

GENERAL INFORMATION:
APPLICANT: Kini, R. Manjunatha
TITLE OF INVENTION: Small Peptides Having Potent Anti-Angiogenic Activity
FILE REFERENCE: 1781-170P

CURRENT FILING DATE: 1999-08-30

EARLIER PILING DATE: 1999-09-04

NUMBER OF SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 31

LENGTH: 14
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Best Local Similarity 100...
Local 14; Conservative
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ORGANISM: mammalian
RESULT 1
US-09-385-442-31
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Sequence 13, Application US/09938391A

Sequence 13, Application US/09938391A

Sequence 13, Application US/09938391A

Sequence 13, Application

Application: Inc. and Pfizer Products, Inc.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING DISORDERS

TITLE OF INVENTION: INVOLVING ANGIOGENESIS

FILE REFERENCE: 315.3.00244, PC10.090A

CURRENT APPLICATION NUMBER: US/09/938,391A

CURRENT APPLICATION NUMBER: US/09/938,391A

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2000-08-25

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn version 3.2

SEQ ID NO 13

TYPE: PRI

TYPE: RESULT 2 US-09-938-391A-13

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Facent No. 6524583
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002582
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF FILING DATE: 1999-04-28
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-561-526-13
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GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 14; Conservative
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Patent No. 634221

GREERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002584
CURRENT FILING DATE: 1200-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 13
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US-09-561-500-13
Sequence 13, Application US/09561500
Fedent No. 6342219
GENERAL INFORMATION:
APPLICANT: Philip B. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTHEODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR PILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOUTHWARE: PatentIn Ver. 2.0
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; Pred. No. 0.00013;
0; Mismatches 0; Indels
                                                                                                                                       Length 184;
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                                                                                                                              Query Match
100.0%; Score 68; DB 4; L
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 14; Conservative 0
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; ORGANISM: MURINE
US-09-938-391A-13
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LENGTH: 191
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100.0%; Score 68; DB 1; Length 195; 100.0%; Pred. No. 0.00014; tive 0; Mismatches 0; Indels
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Pred. No. 0.0016;
1; Mismatches 1; Indels
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Patent No. 6835806
GENERAL INFORMATION
APPLICANT: Phoenix Pharmaceuticals, Inc.
APPLICANT: Chang, Jaw-Kang
TITLE OF INVENTION: Cell Growth Regulation System
FILE REFERENCE: PhoenixPharPull
CURRENT APPLICATION NUMBER: US/09/822,540A
CURRENT FILING DATE: 2001-03-30
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Diskette, 1.44 Mb
COMPUTER: 18M PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
CLIASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/194,561
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: John F. Freeman
REGISTATION UNDMER: 29,066
REFERENCE/DOCKET NUMBER: 00241
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 5, Application US/09315689 ; Patent No. 6346510
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 195
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Best Local Similarity 85.7*
Matches 12; Conservative
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Best Local Similarity 100.
Matches 14; Conservative
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STRANDEDNESS: N/A
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US-08-159-784-2
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US-09-315-689-5
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; Sequence 13, Application US/09561005
; Sequence 13, Application US/09561005
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TILE OF INVENTION: ANTIBODY CONJUGATE METHODS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002585
; CURRENT APPLICATION NUMBER: US/09/561,005
; CURRENT FILING DATE: 1999-04-28
; RIGH APPLICATION NUMBER: 60/131,432
; NUMBER OF SEQ ID NOS: 44
; SOUTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
LENGTH: 191
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TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY
TITLE OF INVENTION: INTIBITING VEGF
TITLE OF INVENTION: INTIBITING VEGF
TITLE OF INVENTION: 1002584
CURRENT PEPLICATION NUMBER: US/09/998,831
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 09/561,108
PRIOR PILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
TYPE: PRI
CURRENT PATENT
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; Patent No. 5643783
; GENERAL INFORMATION: Olsen
; TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF
; NUMBER OF SEQUENCES: 9
; CORRESONDENCES ADDRESS:
ADDRESSEE: Fish & Richardson
; STATE: Massachusetts
; STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Length 182

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GENERAL INCORNATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OP INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002586
CURRENT APPLICATION NUMBER: 108/09/561,526
CURRENT FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEC ID NOS: 44
SOFTWARE: PATCHIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Folkman, Judah
APPLICANT: O'Rellly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                       ) OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC; OTHER INFORMATION: PEPTIDE US-09-561-108-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 59; DB 3; Length 182; Pred. No. 0.0053;
                                                                                                                                                                                         1; Indels
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; OTHER INFORMATION: PEPTIDE
US-09-561-526-14
                                                                                                                                           Score 59; DB Dred, No. 0.009
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; Sequence 14, Application US/09561526
; Patent No. 6416758
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; Sequence 3, Application US/09315689
; Patent No. 6346510
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                               Query Match
Best Local Similarity 85.7%;
Matches 12; Conservative
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Best Local Similarity 85...
Thes 12; Conservative
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Best Local Similarity 85.7
Matches 12, Conservative
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US-09-315-689-3
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SEQ ID NO 14
LENGTH: 182
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APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE ON THE TOTAL THORPE COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002584
CURRENT PILLING DATE: 2000-04-28
FRICH APPLICATION NUMBER: 60/131,432
PRIOR APPLICATION NUMBER: 60/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID 0.14
LENGTH: 182
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Ratent No. 6342219

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002500
CURRENT APPLICATION NUMBER: US/09/561,500
CURRENT FILING DATE: 2000-04-28
RIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
  APPLICANT: Folkman, Judah
APPLICANT: O'Reilly, Michael
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
TITLE OF INVENTION: Therapeutic Antiangiogenic Endostatin Compositions
FILE REFERENCE: 05213-0229
CURRENT APPLICATION NUMBER: US/09/315,689
CURRENT FILING DATE: 1999-05-20
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
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) OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
) OTHER INFORMATION: PEPTIDE
0S-09-561-500-14
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Pred. No. 0.0053;
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Pred. No. 0.0052;
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US-09-561-108-14
Sequence 14, Application US/09561108
Patent No. 6342221
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Best Local Similarity 85.7
Matches 12; Conservative
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Best Local Similarity 85.7
Matches 12, Conservative
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US-09-561-500-14
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LENGTH: 182
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Search completed: March 10, 2005, 11:11:31 Job time : 29.3684 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2005, 10:55:58; Search time 71.1053 Seconds (without alignments) 76.150 Million cell updates/sec Run on:

US-09-766-412-31 68 1 VPIVNLKDEVLSPS 14 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 segs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

genesequi988: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aab74257 Exemplary	Aab80863 Angiostat	Abg97540 Antiangio	Aab35585 Antiangio	Aab49807 Murine en	Aam49504 Mouse end	Aay18409 Endostati	Aay08689 Murine en	Aay70258 Murine an	Aab49380 Murine en	Abg31793 Human end	Abu64290 Murine en	Aab28398 Murine en	Aau77950 Amino aci	Aae02031 Murine en	Aab71930 Murine en	Abb79902 Mouse end	Adn00602 Murine en	Ado43904 Amino aci	Aay08691 Murine ge	Murine	Mouse	Mouse	Aaw92297 Mouse alp	Abo84585 Mouse can
ID	AAB74257	AAB80863	ABG97540	AAB35585	AAB49807	AAM49504	AAY18409	AAY08689	AAY70258	AAB49380	ABG31793	ABU64290	AAB28398	AAU77950	AAE02031	AAB71930	ABB79902	ADN00602	ADO43904	AAY08691	AAY08692	AAY25114	AAW26328	AAW92297	AB084585
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ABO84584 ABG31788 ABG31788 AAC96121 AAX94324 AAU00901 AAU00998 AAX56622 AAX56622 AAX56622 AAX7951 AAV00897 AAV70653 AAY70552 AAX70653	AAB30493
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ALIGNMENTS

RESULT 1

Anti-angiogenesis; plasminogen; VEGF; vascular endothelial growth factor; FLT-1; tumour; metastasis; cancer. Exemplary anti-angiogenic peptide #31. ¥. AAB74257 standard; peptide; 14 01-SEP-2000; 2000WO-SG000131. 99SG-00004310. (UYSI-) UNIV SINGAPORE NAT. (first entry) WO200118030-A2. Homo sapiens. 03-SEP-1999; 23-MAY-2001 15-MAR-2001. AAB74257; AAB74257

Ge R, Kini RM;

WPI; 2001-257785/26.

Peptides comprising a portion of a protein selected from plasminogen, endostatin, VEGF, FLT-1 and KDR/FLK-1 are useful for treating primary tumor growth.

Claim 7; Page 18; 34pp; English.

The present invention relates to anti-angiogenesis peptides from a portion of a selected from plasminogen, endostatin, VEGF or FLT-1. The invention is used to prevent or treat primary tumour growth or metastasis or undesired angiogenesis

Sequence 14 AA;

ö Gaps ö Query Match 100.0%; Score 68; DB 4; Length 14; Best Local Similarity 100.0%; Pred. No. 3.6e-05; Matches 14; Conservative 0; Mismatches 0; Indels

1 VPIVNLKDEVLSPS 14

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AAB80863;

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The invention discloses a peptide comprising a portion of a protein e.g. plasminogen, endostatin (Endo-1-4), vascular endothelial growth factor (VEGF), FLT-1 or kinase insert domain containing receptor/FLK-1. These peptides are able to act as potent angiogenic inhibitors (Angio-1-5) inhibiting endothelial cell proliferation and retarding tumour growth. Angiogenesis is the process of new blood vessel formation from precess of new blood vessel formation from precesses and including endothelial cell proliferation, migration and assembly into tubule structures. It plays an important role in normal physiological functions such as embryonic development and wound healing. Conditions including tumour growth and metastasis, rheumatoid arthritis and psoriasis. Anticancer therapy by inhibiting tumour angiogenesis is called antiangiogenic therapy. VEGF is a endothelial specific mitogen that functions through two high affinity tyrosine kinase receptors, FTT-1 and FLK-1 (not defined). Protein-protein interactions are crucial to many physiological and pharamacological processes and the peptides disclosed interactions. The peptides are useful for preventing or treating undesired angiogenesis and primary tumour growth or metastasis. The sequences presented in ABG97510-ABG97559 are examples of
                                                                                                                                                                                                                                                                                                                                                                          Novel peptide for preventing/treating undesired angiogenesis, has a portion of a protein e.g. plasminogen, endostatin, and potent antiangiogenic activity and endothelial cell proliferation inhibition
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30-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is a peptide which is effective in inhibiting undesirable angiogenesis. Angiogenesis is the process of new blood vessel formation from pre-existing vessels. Inappropriate angiogenesis is associated with various pathological conditions including solid tumour growth and metastasis. The present peptide can be used to to prevent tumour metastasis or inhibit the growth of a primary tumour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides having potent anti-angiogenic activity, useful for the treatment of tumors, comprise a portion of a FLT-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis; plasminogen; endostatin; Endo-; VEGF; vascular endothelial growth factor; FLT-1; kinase insert domain; FLK-1; angiogenic inhibitor; Angio-; endothelial cell; proliferation; tumour growth, blood vessel formation; migration; tubule structure; embryonic development; wound healing; tumour metastasis; rheumatoid arthritis; psoriasis; anticancer; therapy; anticance therapy; anticance therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                 AAB80863 standard; peptide; 14 AA.
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  1 VPIVNLKDEVLSPS 14
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Gene clone of inhibitory factor for hyperplasia of inner blood vessel cells in human body's real tumor, and its use in anti-tumor blood vessel
               of prematurity, macular degeneration, corneal graft rejection, retrolental fibroplasia, rubeosis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include Osler-Webber syndrome, myocardial angiogenesis, plaque neovasculisation, telangiectasia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel preparation which inhibits the proliferation of blood vessel endothelium and prevents the regeneration activity of tumour blood vessels. The preparation can also be used as a biological preparation in the treatment of tumours. This sequence represents the murine endostatin protein described in the invention
 retinopathy
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vessels such as diabetic retinopathy, neovascular glaucoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 68; DB 5; Length 183; 100.0%; Pred. No. 0.00069; arive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.00038;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken; cancer; inflammation; angiogenesis-dependent disease.
                                                                                                                                                                                                                  Polypeptides derived from endostatin exhibiting antiangiogenic activity useful for treatment of angiogenesis-dependent tumors.
                                                                                                                                                                                                                                                                                                             The present invention describes a number of peptides derived from endostratin which exhibit antianglogenic activity. These may be used in the treatment of cancer. The present sequence is one of the peptides of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Pred. No. 0.00016;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                          Claim 3; Page 18; 28pp; English
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               11-APR-2000; 2000WO-EP003236.
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                                                                                      MILANO.
FIRENZE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-040937/05.
                                                                                                                                                                                 WPI; 2001-007005/01.
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200067771-A1
                                                  15-APR-1999;
                                                                                      UYMI-) UNIV
                                                                                                        UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-MAY-1999;
14-JUL-1999;
                                                                                                                                           Chillemi F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                        (UYFI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
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Gaps

Plasminogen, murine; angiostatin; endostatin; gene therapy; vector; anti-angiogenic; attenuation; cytostatic; anti-diabetic; ophthalmology; tumour growth; solid tumour; diabetic retinopathy; retina.

Murine endostatin protein fragment.

(first entry)

10-AUG-1999

AAY08689;

(MASI) MASSACHUSETTS INST TECHNOLOGY.

(GENE-) GENETIX PHARM INC

98WO-US024950. 97US-00975424.

20-NOV-1998; 20-NOV-1997;

WO9926480-A1

Mus sp.

03-JUN-1999.

Bachelot T;

Leboulch P, Pawliuk RJ,

WPI; 1999-357696/30. N-PSDB; AAX77715.

Anti-angiogenic gene therapy vectors.

AAY08689 standard; protein; 184 AA.

AAY08689

69 VPIVNLKDEVLSPS 82

g

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This sequence is the mouse endostatin. The invention relates to a the mutant endostatin (EM), which has anti-angiogenic activity, and is designated EM1. Compositions comprising EM1 or fusion proteins comprising EM1, are useful for treating diseases characterised by angiogenic activity, such as angiogenesis-dependent cancers, benign tumours, cactivity, such as angiogenesis, ocular angiogenesis, Osler-Webber Syndrome, myocardial angiogenesis, plaque neovascularisation, contestinal adhesions, atherosclerosis, scleroderma, hypertrophic scars, cat scratch disease, Helicobacter pylori ulcers, dialysis graft vascular access stenosis, contraception and obesity. In particular, the diseases treatable by EM1 comprise cancer, especially renal cancer. The methods creatable by EM1 comprise cancer, especially renal cancer. The methods provide a means for introducing EM1 into mammalian cells via gene therapy, for production of the EM1 via recombinant means, as well or better than whole endostatin. Use of EM1 protein. EM1 performs as well or better than whole endostatin. Use of EM1 is advantageous for treatment of angiogenic diseases in that increasingly smaller peptides are more potent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  angiogenic diseases in that increasingly smaller peptides are more potent
on a weight basis, and may be able to better penetrate tissues
                                                                                                                                                                                      benign tumour; rheumatoid arthritis; psoriasis; ocular angiogenesis; osler-Webber Syndrome; myocardial angiogenesis; angiofibroma; cancer; plaque neovascularisation; telangiectasia; atherosclerosis; scleroderma; dialysis graft vascular access stenosis; renal cancer; therapy.
                                                                                                                                                                          endostatin; angiogenesis-dependent cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 68; DB 2; Length 184;
Pred. No. 0.0007;
Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mutant endostatin having anti-angiogenic activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (BETH-) BETH ISRAEL DEACONESS MEDICAL CENT.
                AAY18409 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 31; Fig 2; 105pp; English.
                                                                                                                                                                        EM1; anti-angiogenic peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  97US-0067888P.
98US-0082663P.
98US-0108536P.
                                                                                                                                                                                                                                                                                                                                                                                                               98WO-US026057
                                                                                                                                   Endostatin protein sequence.
                                                                                            (first entry)
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Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-385604/32.
N-PSDB; AAX79949.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                 WO9929855-A1.
                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1998;
16-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sukhatme VP;
                                                                                              24-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                      17-JUN-1999
                                                       AAY18409;
                                                                                                                                                                                                                                                                                            Mus sp
AAY18409
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This invention describes a novel viral gene therapy vector comprising a nucleic acid molecule encoding an anti-angiogenic polypeptide chosen from human or murine andiogenic polypeptide chosen from inhibiting fusions and fragments, where the viral vector is sufficiently attenuated for use in human gene therapy. The products of the invention have anti-angiogenic, cytostatic, anti-diabetic and ophthalmological activity. The vector is used in gene therapy for inhibiting tumour growth in humans harbouring a solid tumour. The vector expresses an anti-angiogenic polypeptide. An additional use comprises treatment of diabetic retinopathy, where the anti-angiogenic polypeptide inhibits angiogenesis in the vicinity of the retina. The vector is administered to cells ex vivo and then administered to the patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Murine, immunoglobulin Fc fragment, endostatin, immunofusin, angiogenesis, inhibitor; cytostatic; antirheumatoid; antiathritic; antipsoriatic; antidiabetic; ophthalmological; immunosuppressant; vasotropic; vulnerary; treatment; antiarteriosclerosis; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 68; DB 2; Length 184; 100.0%; Pred. No. 0.0007; Pred. 0; Mismatches 0; Indel8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine angiogenesis inhibitor, endostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY70258 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 6; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 VPIVNLKDEVLSPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VPIVNLKDEVLSPS 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-2000
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AAY70258
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Gaps ; 0

0; Mismatches

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RESULT 8

14

1 VPIVNLKDEVLSPS

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Endostatin peptide comprising at least four endostatin amino acid
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                                                                                   02-MAY-2000; 2000WO-US012063
                                                                                                                     99US-0132907P
                                                                                                                                     99US-00353333
                                                                                                                                                                       (BURN-) BURNHAM INST
                                                                                                                                                                                                                                                                                                                               diabetic retinopathy
                                                                                                                                                                                                                                            WPI; 2001-040937/05.
                                                                                                                                                                                                                                                          N-PSDB; AAC88290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 184 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200268457-A2.
                  WO200067771-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiangiogenic.
                                                                                                                     06-MAY-1999;
14-JUL-1999;
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                                                16-NOV-2000.
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                                                                                                                                                                                                          Vuori K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 agents
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABG31793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a signal sequence, an immunoglobulin For region, an angiogenesis inhibitor selected from angiostatin, endostatin, a plasminogen fragment having angiostatin activity, a collagen XVIII fragment having endostatin activity, or combinations of them. The fusion protein (immunofusin) is used to inhibit angiogenesis and to treat diseases or conditions mediated by angiogenesis. Conditions that may be treated include solid tumours, blood born tumours metastasis, benign tumours including mediated baemangiomas, acoustic neuromas, neurofibromas, trachomas and pyrogenic reaminogathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental collar plane, rubeosis and osler-Webber syndrome; myocardial angiogenesis, plaque neovascularisation, telangiectasia, haemophiliac joints' angiofibroma, wound granulation, and excessive or abnormal stimulation of hypertrophic scars, i.e. keloid scars. The DNA constructs may be used in the construction of immunofusin containing murine immunoglobulin Fc fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                              rel fusion protein of angiostatin or endostatin and an immunoglobulin region, useful for treating conditions mediated by angiogenesis, such rheumatoid arthritis, tumors and macular degeneration.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Endostatin; antiangiogenic; angiogenesis; human; mouse; chicken; cancer; inflammation; angiogenesis-dependent disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The patent discloses a DNA molecule encoding a fusion protein comprising
              ocular angiogenic disease; diabetic retinopathy; macular degeneration; myocardial angiogenesis; plaque neovascularisation; telangiectasia; wound granulation; keloid scar; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 68; DB 3; Length 184; 100.0%; Pred. No. 0.0007; ive 0; Mismatches 0; Indels
metastasis; atherosclerosis; psoriasis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Page 48-49; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB49380 standard; protein; 184 AA.
                                                                                                                                                                                        99WO-US019329
                                                                                                                                                                                                                          98US-0097883P
                                                                                                                                                                                                                                                            (LEXI-) LEXINGEN PHARM CORP.
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                                                                                                                                                                                                                                                                                             Li Y, Gillies SD;
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hes 14; Conservative
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N-PSDB; AAZ51299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 184 AA;
                                                                                                                   WO200011033-A2.
                                                                                   Mus musculus,
                                                                                                                                                                                      25-AUG-1999;
                                                                                                                                                                                                                          25-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2001
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环,
                                                                                                                                                                                                                                                                                                                                                                                 Novel
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Matches
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AAB49380
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The present invention provides endostatin peptides which can be used in the modulation of angiogenesis. This is useful in the treatment of cancers, inflammation, rheumatoid arthritis, chronic articular rheumatism, psoriasis, disorders associated with inopportune invasion of prematurity, ascular degeneration, corneal graft rejection, retrolental fibroplasia, tubososis, capillary proliferation in atherosclerotic plaques and osteoporosis. Other angiogenesis-dependent diseases include osler-webber syndrome, myocardial angiogenesis, plaque neovasculisation, telangiectasia, haemophiliac joints and wound granulation. In addition, the peptides can be used as birth control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 4; Length 184; Pred. No. 0.0007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; endostatin; tumour; cancer; metastasis; cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chillemi F, Vicentinie LMT, Francescato P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABG31793 standard; protein; 184 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Sci
100.0%; Pr
tive 0; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human endostatin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-FEB-2002; 2002WO-IT000119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-FEB-2001; 2001IT-MI000394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Conservative
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Best Local Similarity
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Gaps

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The present invention relates to anti-Vascular Endothelial Growth Factor (VEGF) antibodies that bind to the same epitope as the monoclonal antibody ATCC FPA 1595 and which significantly inhibit VEGF binding to the VEGF receptor VEGFRI, without inhibiting VEGF binding to the VEGF receptor VEGFRI. The present sequence is murine endostatin. Endostatin any be conjugated onto the anti-VEGF antibodies of the present invention. The anti-VEGF antibodies of the present invention are useful for the treatment and diagnosis of cancer, especially vascularised solid tumours
neovascularisation, choroidal neovascularisation, retinal neovascularisation, age-related macular degeneration, visual impairment, occular dysfunction, loss of vision, retinopathy, or blindness in a human. The present sequence is a protein shown in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunogenic composition for the treatment and diagnosis of cancer comprises an anti-VEGF (vascular endothelial growth factor) antibody binding the same epitope as the monoclonal antibody ATCC PTA 1595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine; endostatin; cytostatic; antiproliferative; vascular endothelial growth factor; VEGF; antibody; VEGF2 receptor; cancer; vascularised solid tumour.
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                                                                                                                                                                            100.0%; Score 68; DB 7; Length 184; 100.0%; Pred. No. 0.0007;
                                                                                                                                                                                                                       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 10; Page 290-291; 298pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         AAB28398 standard; protein; 191 AA.
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                                                                                                                                                                                                                                                                   1 VPIVNLKDEVLSPS 14
                                                                                                                                                                                                                                                                                                69 VPIVNLKDEVLSPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                          14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thorpe PE, Brekken RA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687317/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                     Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine endostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAC67777
                                                                                                                                   Sequence 184 AA;
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                                                                                             invention
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                                                                                                                                                                                                                          Matches
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AAB28398
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0
                                                                    New peptide useful for the preparation of medicaments with antianglogenic activity that may be used in treating tumors or metastases, comprises a sequence corresponding to fragments of human endostatin.
                                                                                                                                                                                                                   sequences corresponding to the human endostarin polypeptide sequence, its salt or non-toxic derivative. The peptides are useful in the preparation of medicaments with antianglogenic activity which may be useful in treating tumours or metastages. This sequence represents a human endostatin polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to an adeno-associated viral (AAV) vector comprising a polynucleotide that comprises a nucleic acid segment that encodes a choroidal or ocular neovascularisation inhibitory polypeptide operably linked to a promoter that expresses the segment to produce the polypeptide in a selected mammalian host cell. Such a vector is useful for providing a choroidal or coular neovascularisation inhibitory polypeptide to a mammal, for use in the therapy of ocular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel adeno-associated viral vector comprising polynucleotide encoding pigment epithelium-derived factor, useful for treating choroidal neovascularization, blindness, loss of vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                     The invention relates to peptide comprising 20-50 amino acids with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vector, rAAV, recombinant adeno-associated viral vector, anti-angiogenesis, PEDF; angiogenesis, eye disorder, blindness, retinal degeneration, macular degeneration, neovascularisation,
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                  Length 184;
                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 5; Lengtn 10-
Pred. No. 0.0007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABU64290 standard; protein; 184 AA.
                                                                                                                                                            Disclosure; Fig 1; 24pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 38; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Campochiaro PA,
                                                                                                                                                                                                                                                                                                                                                                                                    100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                         100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-MAR-2003; 2003WO-US008667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-MAR-2002; 2002US-0366114P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYFL ) UNIV FLORIDA RES FC
(UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69 VPIVNLKDEVLSPS 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VPIVNLKDEVLSPS 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Murine endostatin protein.
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-779243/73.
N-PSDB; AAL56259.
                           WPI; 2002-698655/75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ophthalmological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003080648-A2.
                                                                                                                                                                                                                                                                                                                                                           Sequence 184 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-2004
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ABU64290;

RESULT 12 ABU64290

à 셤 Mus sp.

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Gaps

; 0

Indels

; 0

Murine, endostatin, fusion protein, nucleotide-binding domain, NBD; ligand-binding domain, LBD; transcription regulating domain, TRD; cancer; zinc finger protein; ZFP; ligand-activated transcriptional regulator; gene regulation; gene therapy; cell proliferative disorder; psoriasis;

Murine endostatin fused to N-terminal secretion signal

31-JUL-2001 (first entry)

AAE02031;

AAE02031 standard; protein; 207 AA.

RESULT 15 AAE02031

89

76 VPIVNLKDEVLSPS

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1 VPIVNLKDEVLSPS 14

pemphigus vulgaris; Behcet's syndrome; lipid histiocytosis.

Beerli R;

Barbas CF, Kadan M, 2001-308618/32. N-PSDB; AAD06108

(NOVS) NOVARTIS AG. (SCRI) SCRIPPS RES INST.

23-OCT-2000; 2000WO-EP010430 25-OCT-1999; 99US-00433042. 02-JUN-2000; 2000US-00586625.

WO200130843-A1. 03-MAY-2001.

Mus sp.

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Mouse; immunoconjugate; anti-vascular endothelial growth factor antibody; anti-vEGF antibody; menoclonal antibody 203 ATCC PTA 1595; VEGF receptor; VEGFR2; KDK/FIk-1; VEGFR1; FIL-1; angiogenesis; mecular degeneration; ocular neovascular disease; cancer; vascularised solid tumour; AIDS; metastatic tumour; endothelial cell proliferation; inflammatory disorder; actheroselerosis; diabetic retinopathy; corneal graft rejection; acquired immune deficiency syndrome; infection; restenosis; fungal ulcer; sickle cell anaemia; endometriosis; endostatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoconjugate compositions for treating cancer by inhibiting angiogenesis and for delivering a diagnostic agent to tumor, comprises anti-vascular endothelial growth factor antibody attached to a biological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 10; Page 11-12 (Sequence listing); 299pp; English.
                                                                                                Amino acid sequence for mouse endostatin.
                        AAU77950 standard; protein; 191 AA.
                                                                                                                                                                                                                                                                                                               12-OCT-2001; 2001AU-00079401
                                                                                                                                                                                                                                                                                                                                      28-APR-2000; 2000AU-00048049
                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                              (TEXA ) UNIV TEXAS SYSTEM
                                                                                                                                                                                                                                                                                                                                                                                      Thorpe PE, Brekken RA;
                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-281368/33.
N-PSDB; ABK47719.
                                                                                                                                                                                                                                                            AU200179401-A.
                                                                        02-JUL-2002
                                                                                                                                                                                                                                                                                     06-DEC-2001
                                               AAU77950;
                                                                                                                                                                                                                                     Mus sp.
RESULT 14
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The present invention relates to antibody-based compositions comprising an immunoconjugate such as anti-vascular endothelial growth factor (VEGF) antibody (Ab) (or its antigen-binding fragment), attached to a biological agent, where the Ab binds to the same epitope as the monoclonal antibody (MAD) 2C3 ATCC PTA 1595, and significantly inhibits VEGF binding to the VEGF receptor VEGFR2 (KDK/Flk-1) without inhibiting VEGF binding to the VEGF receptor VEGFR2 (KDK/Flk-1) without inhibiting vEGF binding to the VEGF receptor VEGFR2 (KDK/Flk-1). The compositions of the invention are useful in therapy, and diagnosis, for inhibiting angiogenesis in an inmial having ocular neovascular disease or macular degeneration, and for delivering a biological agent to a vascularised tumour. The compositions can also be used for treating cancer and subjects at risk of developing, a vascularised solid tumour, a metastatic tumour or metastases from a primary tumour. The composition is useful for specifically inhibiting to VEGF-induced endothalial cell proliferation, without significantly inhibiting to VEGF-induced endothalial cell proliferation, without significantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibiting VEGF-induced macrophage, osteoclast or chondroclast function. The compositions can be used for treating various diseases such as inflammatory disorders, atherosclerosis, diabetic retinopathy. restenosis, acquired immune deficiency syndrome (AIDS), blood borne tumours, corneal graft rejection, Crohn's disease, fungal ulcers, infections, sickle cell anaemia, and endomerriosis. The present sequence represents mouse endostatin. Endostatin may be attached or functionally associated with anti-VEGF antibodies
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.. 0

Match 100.0%; Score 68; DB 5; Length 191; Local Similarity 100.0%; Pred. No. 0.00073; les 14; Conservative 0; Mismatches 0; Indels

Sequence 191 AA;

Query Match

Best Local Matches

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New fusion protein containing nucleotide-binding and ligand-binding domains, useful e.g. in gene therapy of cancer, provides ligand-activated control of gene expression.
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100.0%; Score 68; DB 4; Length 207;
Best Local Similarity 100.0%; Pred. No. 0.0008;
Matches 14; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                          Example 19; Page 209; 218pp; English.
                                                                                                                                                                                                                                                                                                                          Sequence 207 AA;
                                                                                                                                                                                                                                                                                                               regulators
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                                                                                                                                                                                                                                                                                                                                           Gaps
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The invention relates to fusion protein comprising a nucleotide-binding domain (NBD), a ligand-binding domain (LBD) of an intracellular receptor (ICR) and a transcription regulating domain (TBD). NBD is a polydactyl cancer finds a protein (ZFP), or a modular part of it, that interacts specifically with a contiguous sequence of at least 3 nucleotides. The fusion protein functions as a ligand-activated transcriptional regulator. The fusion protein and the nucleic acid encoding it, are used to regulate gene expression, particularly in gene therapy for treating malignant cell proliferative diseases (e.g. psoriasis, proliferative diseases (e.g. psoriasis, penphigus vulgaris, Behcet's syndrame and lipid histocytosis). The fusion protein and its DNA are also useful for treating diseases caused by virues in humans/plants, genetic and/or acquired diseases. The fusion protein can be designed to target any selected gene (endogenous or exogenous), and can be made to have different selectivity or specificity for endogenous or exogenous is not expensed in the present sequence is murine for endogenous and the manner for expense to the present sequence is murine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endostatin fused to an N-terminal secretion signal. The corresponding CDNA sequence was used in the construction of Left end shuttle plasmids containing regulatable transgene cassettes for evaluation of Cys2-His2 Zinc finger DNA binding domain (DBD)-Oestrogen receptor (ER) LBD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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1 VPIVNLKDEVLSPS 14 ||||||||||||| 92 VPIVNLKDEVLSPS 105

Search completed: March 10, 2005, 11:06:52 Job time : 72.1053 secs

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Sequence 115, Applications of the sequence 1, Applications of 
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                                                                                                                                                                                                                                                                                                March 10, 2005, 11:07:00 ; Search time 79.0263 Seconds (without alignments) 54.260 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-873-676-115

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US-09-105-11-1

US-10-131-24-1

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US-10-042-347-1

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Sequence 16, Appl Sequence 18, Appl Sequence 13, Appl Sequence 13, Appl Sequence 13, Appl Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 14, Appl Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 11, Appli
14 US-10-131-241-46 14 US-10-292-418-18 13 US-10-926-820-13 13 US-10-936-820-13 14 US-10-936-831-13 19 US-09-998-831-13 19 US-09-998-831-13 19 US-09-373-561-13 19 US-09-373-561-13 19 US-10-080-797-3 14 US-10-131-241-6 14 US-10-131-241-55 14 US-10-131-241-55 14 US-10-131-241-55 14 US-10-131-241-55 14 US-10-131-241-55 15 US-09-998-831-14 16 US-10-131-241-55 17 US-10-131-241-55 18 US-09-998-831-14 19 US-10-131-241-55 19 US-09-998-831-14 19 US-10-131-241-55 19 US-09-998-831-14 19 US-10-131-241-55 11 US-10-131-241-55 12 US-09-978-831-14 13 US-10-99-88-81-11 14 US-10-131-241-52 15 US-09-978-531-1 16 US-10-920-418-4 17 US-10-920-418-4 18 US-10-920-418-4 19 US-10-920-418-4 19 US-10-920-418-4 19 US-10-920-418-4 11 US-10-920-418-4 11 US-10-920-418-4 12 US-10-920-920-12
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ALIGNMENTS

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RESULT'1

SEQUENCE 30, Application US/09766412

SEQUENCE 30, Application US/09766412

SEQUENCE 30, Application US/09766412

SEQUENCE 30, Application US/09766412

PRICE WOUND SEQUENCE 30 SEQUENCE 30
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Gaps
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Sequence 1, Application US/09405499

Sequence 1, Application US/09405499

Patent No. USZ0020123458A1

APPLICANT: NEORANTION:

APPLICANT: POlkman, M. Judah

TITLE OF INVENTION: Folkman, M. Judah

TITLE OF INVENTION: Folkman, N. Judah

FILE REFERENCE: 05213-0640

CURRENT FILING DATE: 1999-09-23

NUMBER OF SEQ ID NOS: 3

SOFTWARER: PATENCE: 1999-09-23

SOFTWARER: PATENCE: 2.0

SEQ ID NO 1

LENGTH: 20
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                                                                                                          Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 66; DB 9; Length 20;
Pred. No. 0.00015;
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Patent No. US20020127595A1

GRENERAL INFORMATION

APPLICANT: O'Reilly, Michael S.

APPLICANT: FOlkman, M. Judah

TITLE OF INVENTION: Mechads of Detecting Endostatin Protein

FILE REPERENCE: 05213-0227
                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                        Score 66; DB 9;
Pred. No. 0.00015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 66; UB Best Local Similarity 100.0%; Pred. No. 0.0º
                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/174,516A CURRENT FILING DATE: 1998-10-16 NUMBER OF SEQ ID NOS: 2 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
US-09-154-302-1
; Sequence 1, Application US/09154302
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                                                                                                        100.0%;
                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                  1 OPVLHLVALNTPL 13
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Best Local Similarity 100.
Matches 13; Conservative
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                            ORGANISM: Murine
; TISSUE TYPE: Collagen
US-09-174-282-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Murinae gen. sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Murinae gen. sp.
            ORIGINAL SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-174-516-1
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APPLICANT: MacDonald, Nicholas J.
APPLICANT: Sim, Kim L.
TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use FILE REFERENCE: 05213-0378 (43170-259333)
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 60/209,065
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-02
PRIOR FILING DATE: 2000-06-08
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Batentin Version 3.1
ENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                        Length 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: PAETENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE:
FLING PRICATION NUMBER: US 09/174, 282
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
APPLICATION NUMBER: US 08/740,168
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFRENCE/DOCKET NUMBER: 0521:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3700
TELEFAX: 404-818-3799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   internal
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                            ; ORGANISM: mammalian
US-09-873-676-115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Georgia
: USA
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ANTI-SENSE: N
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Gaps
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Publication No. US20030087393A1
GENERAL INFORMATION:
PPLICANT: O'Reilly, Michael
Folkman, M. Judah
TITLE OF INVENTION: Therapeutic Antiangiogenic Compositions
and Methods
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                                                                                                                                                                                                                         Length 20;
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                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/232,316
                                                                                                                                                                                                                         100.0%; Score 66; DB 14;
100.0%; Pred. No. 0.00015;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 03-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION UNDER: US/08/740,168A
FILING DATE: 22-CT-1996
ATTORNEY/AGENT INFORMATION:
NAME: Warren, William L.
REGISTRATION NUMBER: 36,714
REFERENCE/DOCKET NUMBER: 05213-0223
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & Askew, LLP
STREET: 191 Peachtree, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Murine
IISSUE TYPE: Collagen
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 43
LENGTH: 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 30303
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE: internal ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                             7 QPVLHLVALNTPL 19
                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                 1 OPVLHLVALNTPL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Atlanta
STATE: Georgia
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                     ) ORGANISM: Murinae sp. US-10-131-241-43
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Best Local Similarity
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US-10-232-316-1
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Publication No. US20030012792A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Holaday, John W.
TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
FILE REFERENCE: 05213-0344 43170-271565
CURRENT APPLICATION NUMBER: US/10/131,241
CURRENT FILING DATE: 2002-07-22
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                  GENERAL INFORMATION:
APPLICANT: O'Reilly, Michael
APPLICANT: Folkman, M. Judah
TITLE OF INVENTION: Therapeutic Antiangiogenic Compositions
TITLE OF INVENTION: and Methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 20;
                                                                                                                                                                                                                                                                                 ZIP: 30303
ZIP: 30303
ZIP: 30303
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/154,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match 100.0%; Score 66; DB 9; I
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 13; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: WATER, WILLIAM L.
REGISTRATION NUMBER: 36,714
REGISTRATION NUMBER: 0513-0223
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-818-3709
TELEPHONE: 404-818-3799
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TYPE: amino acid
STRANDEDNESS: single
TYPE: Innear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR APPLICATION NUMBER: US 09/316,802
PRIOR FILING DATE: 1999-05-21
                                                                                                                                         CITY: Atlanta Screen, 11P STREET: 191 Peachtree, 37th Floor CITY: Atlanta STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/740,168
FILING DATE: 22-OCT-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE: internal ORIGINAL SOURCE: ORGANISM: Murine TISSUE TYPE: Collagen
                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jones & A
  Patent No. US20020155987A1
                                                                                                                                                                                                                                                  Georgia
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-131-241-43
                                                                                                                                                                                                                                                                     COUNTRY:
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Sequence 3, Application US/10607501
| Sequence 3, Application US/10607501
| Publication No. US20040091465A1
| GENERAL INFORMATION:
| APPLICANT: Yim, Zachary
| TITLE OF INVENTION: Therapeutic Antiangiogenic Compositions and Methods
| FILE REFERENCE: 05213-0791 (43170-286879)
| CURRENT APPLICATION NUMBER: US/10/607,501
| CURRENT PILING DATE: 2003-06-26
| PRIOR APPLICATION NUMBER: US 60/391,630
| PRIOR PILING DATE: 2002-06-26
| NUMBER OF SEQ ID NOS: 3
| SOFTWARE: Patentin version 3.2
| LENGTH: 20
                                                                                                                             Gaps
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Publication No. US20040102372A1

GENERAL INFORMATION:

APPLICANT: O'Reilly, Michael S.

APPLICANT: Folkman, M. Judah

TITLE OF INVENTION: Methods of Detecting Endostatin Protein

FILE REFERENCE: 05213-0320 (43170-282919)

CURRENT FILING DATE: 2003-02-04

PRIOR FILING DATE: 1995-10-23

PRIOR FILING DATE: 1995-10-23

PRIOR PILING DATE: 1996-09-17

PRIOR PELING DATE: 1996-09-17

PRIOR FILING DATE: 1996-09-17

PRIOR FILING DATE: 1996-09-17

PRIOR FILING DATE: 1996-10-22

PRIOR FILING DATE: 1998-10-16
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                                                             Length 20;
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                                                                                                                             0; Indels
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100.0%; Pred. No. 0.00015;
tive 0; Mismatches 0;
                                                      100.0%; Score 66; DB 15;
100.0%; Pred. No. 0.00015;
cive 0; Mismatches 0;
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SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 OPVLHLVALNTPL 13
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                                                                                                                                                                                             1 OPVLHLVALNTPL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT; ORGANISM: Murinae gen. sp. US-10-607-501-3
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                                                                                                                          13; Conservative
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Best Local Similarity 100.
Matches 13; Conservative
                                                             Query Match
Best Local Similarity
Matches 13; Conserv
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US-10-351-284-1
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Sequence 1, Application US/10042347

Publication No. US20030114370A1

Publication No. US20030114370A1

APPLICANT: PROFMATION:

APPLICANT: Prolkman, M. Judah

TITLE OF INVEXTION: Thereof

FILE REFERENCE: 05213-0880 (43170-249874)

CURRENT PAPLICATION NUMBER: US/17/0/042,347

CURRENT PELING DATE: 1990-05-20

PRIOR APPLICATION NUMBER: US (09/315,689)

PRIOR APPLICATION NUMBER: US (01/06,343)

PRIOR FILING DATE: 1998-09-16

PRIOR FILING DATE: 1998-09-16

PRIOR FILING DATE: 1996-10-23

PRIOR FILING DATE: 1996-10-23

PRIOR APPLICATION NUMBER: US (0/005,835)

PRIOR PRILING DATE: 1996-09-16

PRIOR FILING DATE: 1996-08-02

PRIOR APPLICATION NUMBER: US (0/002,070)

PRIOR PRILING DATE: 1996-09-17

PRIOR PRILING DATE: 1996-09-17

PRIOR FILING DATE: 1996-09-17

PRIOR FILING DATE: 1996-09-17

NUMBER OF SEQ ID NOS: 6

SEGO ID NOS: 
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Publication No. US20030219426A1

GENERAL INFORMATION:

APPLICANT: O'Reilly, Michael S.

APPLICANT: O'Reilly, Michael S.

APPLICANT: POlkman, M. Judah

TITLE OF INVENTION: Therapeutic Antiangiogenic Compositions and Methods

FILE REFERENCE: 05213-3051 (43170-282623)

CURRENT APPLICATION NUMBER: US 60/005,835

PRIOR FILING DATE: 1995-10-23

PRIOR FILING DATE: 1996-08-02

PRIOR FILING DATE: 1996-09-17

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PatentIn version 3.1

SEQ ID NO: 1

LENGTH: 20

TWOS: 100
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   Indels
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0; Mismatches
                                                                                                                             7 OPVLHLVALNTPL 19
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13; Conservative
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ORGANISM: Murinae gen. sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Murinae sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-042-347-1
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   Matches
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APPLICANT: Li, Yue
APPLICANT: Li, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REPERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT APPLICATION NUMBER: US/10/292,418
FRICR APPLICATION NUMBER: 09097,883
FRICR APPLICATION NUMBER: US 60/097,883
FRICR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
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100.0%; Pred. No. 0.0016;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0
Matches 13; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QPVLHLVALNTPL 13
Lo, Kin-Ming
                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Mus musculus
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                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 18
LENGTH: 184
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Sequence 46, Application US/10131241

Sequence 46, Application US/10131241

Publication No. US20330012792A1

SEQUENCE 46, Application US/10131241

Publication No. US20330012792A1

APPLICANT: Holaday, John W.

APPLICANT: Holaday, John W.

APPLICANT: Fortier, Anne H.

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION: Compositions and Methods for Inhibiting Endothelial Cell Prolifer

TITLE OF INVENTION WUMBER: US 09/10/131,241

CURRENT APPLICATION NUMBER: US 09/116,049

FRIOR FILING DATE: 1999-10-06

PRIOR APPLICATION NUMBER: US 09/316,802

FRIOR FILING DATE: 1998-05-21

FRIOR FILING DATE: 1998-05-21

FRIOR PILING DATE: 1998-05-22

NUMBER OF SEQ ID NOS: 65

SSOUTHARE: PatentIn version 3.1

LENGTH: 184
                                                                                                                                                         Sequence 3, Application US/08373938

Publication No. US20020115202A1

GENERAL INFORMATION:
APPLICANT: Hallenbeck, Paul
APPLICANT: Hallenbeck, Paul
APPLICANT: Chen, Cheauyun Theresa
TITLE REFERENCE: 4-30899P1
CURRENT APPLICATION NUMBER: US/09/373,938
CURRENT FILING DATE: 1999-08-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 66; DB 9; Length 42; Best Local Similarity 100.0%; Pred. No. 0.00032; Matches 13; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 QPVLHLVALNTPL 42
                               OPVLHLVALNTPL 19
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1 QPVLHLVALNTPL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Mus musculus US-09-373-938-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Murinae sp. US-10-131-241-46
                                                                                                                     RESULT 13
US-09-373-938-3
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2005, 10:59:54 ; Search time 52.3421 Seconds
 (without alignments)
127.183 Million cell updates/sec Run on:

US-09-766-412-30 66 Title: Perfect score:

1 QPVLHLVALNTPL 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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		Description	Q61434 mus musculu	Qenzk9 mus musculu	Q6ply4 mus musculu	P39061 mus musculu	Q8wxi5 homo sapien	homo	homo	homo	gallu	P39060 homo sapien	Q6rz39 homo sapien	homo	Q9qzd2 rattus norv	Q6p3m9 xenopus tro	Q6dfr4 xenopus tro		Ogeddg mus musculu	Q9wuw5 rattus norv	Osghl9 xenopus lae		Q9b6q6 eriosoma la	Q8awc6 brachydanio	Q9y4w4 homo sapien			Q9b6p8 geoica utri	Q9b6g9 tetraneura	P32333 saccharomyc	Q6ekw7 xenopus lae	Q6nrx7 xenopus lae	Q86sc8 ciona intes
SUMMARIES		ΩI	061434	Q6NZK9	Q6P1Y4	CAIH_MOUSE	QBWXIS	Q8NG19	Q8N4S4	Q6RZ41	093419	CAIH HUMAN	Q6R239	Q6RZ40	Q9QZD2	Ферзм 9	Q6DFR4	035206	Q9EQD9	Q9WUW5	ОВОНГЭ	Q8JFF7	09ве0е	QBAWC6	Q9Y4W4	CA1E_HUMAN	Q7YH34	Q9B6P8	Q9B6G9	MOT1_YEAST	Q6EKW7	Q6NRX7	Q86SC8
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		Score	99	99	99	99	62	62	62	62	62	62	62	62	61	61	61	59	59	54	52	20	45	45	45	44	43	43	43	43	42	42	42
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Q6frv8 candida gla Q921n7 mus musculu Q9b6h6 rhopalosiph Q7ygd1 pemphigus p Q7yh33 periphyllus Q9b6g3 thelaxes su Q9b6g4 tuberolachn Q9b6h8 schizaphis Q9b6h8 phylloxera Q9b6h9 phylloxera Q9b6i0 pemphigus s Q9b6i2 panaphis ju Q9b6i5 pemphigus b
QEFRV8 Q921N7 ATPE RHOPD Q7Y511 Q7Y433 Q9B6G3 Q9B6G4 Q9B6H4 Q9B6H9 Q9B6H9 Q9B6H9 Q9B612
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### ALIGNMENTS

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OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
OS-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Procollagen, type XVIII, alpha 1.
Name=Collaal;
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musnae.
                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
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                                                                                                                  Created)
Last sequence update)
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                                                            PRT; 1140 AA.
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                                                            PRELIMINARY;
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                                                                                                                                                                                                       Collagen (Fragment).
Name=Coll5al;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                  NCBI TaxID=10090;
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RESULT 1
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1D Q61434:
DT 01-M
DT
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060ZK9
1D 060ZK3
AC 060ZK2
DT 05-JJ
DT 05-JJ
DE Procy
GN Name
CO EUKar
OC EUKar
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STRAIN=C57BJ/6; TISSUE=Brain;

MEDLINE=2538257; PubMed=1247932; DOI=10.1073/pnas.242603899;

A Straubberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Alschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T. Max S.I., Wang J., Haieh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

N. Helton D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabs R.A.,

Rahesley W., Helton E., Ketteman M., Madan A., Robrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human
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R GO; GO:0005604; C:basement membrane; IDA.

GO; GO:0005604; C:basement membrane; IDA.

GO; GO:0001525; C:extracellular space; TAS.

R GO; GO:0001525; P:extracellular space; TAS.

R GO; GO:0001525; P:endothelial cell morphogenesis; IDA.

R GO; GO:0001886; P:endothelial cell morphogenesis; IDA.

R GO; GO:0001886; P:positive regulation of eapoptosis; IDA.

R GO; GO:000335; P:positive regulation of cell migration; IDA.

R GO; GO:000884; P:positive regulation of cell migration; IDA.

R InterPro; IPR008161; Clapelix.

R InterPro; IPR008161; Clapelix.

R InterPro; IPR001515; Endostatin.

R Pfam; PF06482; Endostatin.

R Probon: PF004007; Clapen; 7.

R Probon: PF004007; Clapelix; 1.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Procollagan, type XVIII, alpha 1.
Numec-Collagan; (Mouse).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.; Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1138 QPVLHLVALNTPL 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.
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NCBI_TaxID=10090;
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RECURESUB-Embryo,

RECURESOB-Embryo,

RECURESOB-Embryo,

RECURES-2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RECURES-2288257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Alausner R.D., Colling F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Habt N.K.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

REA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

REA DIATCHON M.J., Osores M.B., Doshiyuki S., Carninci P., Prange C.,

Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Roberson R.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA S. Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RY, Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Rodriguez A.C., Grimwood J., Gromutz J. Dickson M.C.,

RA Noring M. I., Skalska U., Smailus D.E., Schnerch A., Scheln J.E.,

RODRS S.J., Marra M.A.,

RA Goneration and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Strausberg R.;
Straus
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 66; DB 2; Length 1315; 100.0%; Pred. No. 0.0062; ive 0; Mismatches 0; Indels 0
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Event=Alternative splicing; Named isoforms=3;
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EMBL, U34608, AACS2901.1, U
EMBL, U34609, AACS2901.1, U
EMBL, U34610, AACS2901.1, U
EMBL, U34611, AACS2901.1, U
EMBL, U34613, AACS2901.1, U
EMBL, U34613, AACS2901.1, U
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AAC52903.1;
AAC52903.1;
AAC52903.1;
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AAC52902.1;
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AAC52902.1;
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AAC52902.1;
AAC52902.1;
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AAC52902.1;
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AAC52901.1
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U03715;
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U34613;
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U03716;
U03718;
U34607;
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U34607;
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U34609;
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U34611;
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EMBL;
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EMBL;
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Rehn M., Pihlajaniemi T.;
"Identification of three N-terminal ends of type XVIII collagen chains and tissue-specific differences in the expression of the corresponding transcripts. The longest form contains a novel motif homologous to rat and Drosophila frizzled proteins.";
J. Biol. Chem. 270:4705-4711(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Liver;
MEDLINE-94240111; PubMed=8183893;
MEDLINE-94240111; PubMed=8183893;
Oh S.P., Kamagata Y., Muragaki Y., Timmons S., Ooshima A., Olsen B.R.;
"Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xaa-Yaa repeats identify a distinct family of collagenous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οŧ
         Rehn M.V., Hintikka E., Pihlajaniemi T.,
"Primary structure of the alpha 1 chain of mouse type XVIII collagen,
partial structure of the corresponding gene, and comparison of the
alpha 1(XVIII) chain with its homologue, the alpha 1(XV) collagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF ENDOSTATIN.
MEDLINE=981469382; PubMed=9501087; DOI=10.1093/emboj/17.6.1656;
Hohenester E., Sasaki T., Olsen B.R., Timpl R.;
"Crystal structure of the angiogenesis inhibitor endostatin at 1.5-A
                                                                                                                                                                                                                                                                                                                                             Rehn M.V., Pihlajaniemi T.; "Alpha 1(XVIII), a collagen chain with frequent interruptions in the collagenous sequence, a distinct tissue distribution, and homology with type XV collagen.";
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MEDLINE=97160848; PubMed=9008168; DOI=10.1016/S0092-8674(00)81848-6;
O'Reilly M.S., Boehm T., Shing Y., Fukai N., Vasios G., Lane W.S.,
Flynn E., Birkhead J.R., Olsen B.R., Folkman J.;
"Endostatin: an endogenous inhibitor of angiogenesis and tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative promoter;
Comment=2 isoforms, 1 (shown here) and 3, are produced by use
alternative promoters;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1591-1774 FROM N.A.
MEDLINE=21217748; PubMed=11321448;
Jia S., Zhu F., Li H., He F., Xiu R.-J.;
"Anticancer treatment of endostatin gene therapy by targeting tumor neovaeculature in C57/BL mice.";
Clin. Hemorheol. Microcirc. 23:251-257(2000).
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-!- FUNCTION: Endostatin potently inhibits endothelial cell
proliferation and angiogenesis. May inhibit angiogenesis by
binding to the heparan sulfate proteoglycans involved in growth
factor signaling.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
MEDLINE=56435922; PubMed=8838808; DOI=10.1006/geno.1996.0139;
Rehn M., Hintikka B., Pihlajaniemi T.;
"Characterization of the mouse gene for the alpha-1 chain of type "Characterization of the reveals that the three variant N-terminal polypeptide forms are transcribed from two widely separated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIFICITY.
MEDLINE=95181468; PubMed=7876242; DOI=10.1074/jbc.270.9.4705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-562 FROM N.A. (ISOFORMS 1 AND 3), AND TISSUE
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Proc. Natl. Acad. Sci. U.S.A. 91:4229-4233(1994)
                                                                                                                                                                                                                                                                                                         SEQUENCE OF 1-1387 FROM N.A. (ISOFORM 3) MEDLINE=94240112; Pubmed=8183894;
                                                                                                        Biol. Chem. 269:13929-13935(1994)
MEDLINE=94245707; PubMed=8188673;
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                                                                                                                                                                                                                                                                       Genomics 32:436-446(1996).
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EMBO J. 17:1
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proteins.

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                                                                                                                                                                                                                                                                     -!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- SIMILANTY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.
-!- SIMILANTY: Contains 1 frizzled (FZ) domain.
Name=1; Synonyms=NCI-764;
IsoId=P39061-3; Sequence=Displayed;
Name=2; Synonyms=Long, NCI-517,
IsoId=P39061-1; Sequence=VSP 008303;
Note=Produced by alternative=splicing of isoform 1;
Name=3; Synonyms=Short, NCI-301;
IsoId=P39061-2; Sequence=VSP 001157, VSP 001158;
TISSUE SPECIFICITY: Expressed in liver, kidney, lung, skeletal muscle and testis.
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PDB; IDYO; X-ray; A=1340-1527.

PDB; IDXI; X-ray; A=1340-1527.

PDB; IKOE; X-ray; 0=1350-1521.

MGD; MGI:88451; Coll8a1.

GO; GO:0005604; C:basement membrane; ID

GO; GO:001552; P:anglogenesis; IMP.
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InterPro; IPR008160; Conlagen.
InterPro; IPR008985; Cona like_lec_gl.
InterPro; IPR010363; DUF959.
InterPro; IPR010515; Endostatin.
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EMBL; U34609; AACS2903.1; JOINED.
EMBL; U34610; AACS2903.1; JOINED.
EMBL; U34611; AACS2903.1; JOINED.
EMBL; U34612; AACS2903.1; JOINED.
EMBL; U34612; AACS2903.1; JOINED.
EMBL; U34613; AACS2903.1; JOINED.
EMBL; U11636; AACS2903.1; JOINED.
EMBL; U11636; AACS2179.1; -.
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EMBL; AF416592; AAL37720.1; -. HSSP; P39060; 1BNL. Pfam; PF06482; Endostatin; 1.
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SEQUENCE
                                                                                                                                         Query Match
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Q8N4S4;
                                                                                                                                                                                                                                                                                                                                                                                Q8NG19;
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"Inhibition effect in vitro of purified endostatin expressed in Pichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                             3D-structure; Alternative promoter usage; Alternative splicing; Cell adhesion; Collagen; Direct protein sequencing; Extracellular matrix; Glycoprotein; Hydroxylation; Repeat; Signal;
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Triple-helical region 1 (NC1).
Triple-helical region 2 (NC2).
Nonhelical region 2 (NC2).
Triple-helical region 3 (COL2).
Triple-helical region 3 (COL3).
Triple-helical region 4 (COL4).
Triple-helical region 4 (COL4).
Triple-helical region 5 (NC5).
Triple-helical region 5 (NC5).
Triple-helical region 6 (NC5).
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Triple-helical region 7 (COL7).
Nonhelical region 8 (NC8).
Triple-helical region 8 (COL8).
Nonhelical region 9 (NC9).
Triple-helical region 9 (NC9).
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                                                                                                                                                                                                                                                                                                                                           Potential.
Collagen alpha 1(XVIII) chain.
Endostatin.
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Feng Y., Wu Y., Zhu X., Liu C.X., Ma Q.J.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBWXIS PRELIMINARY; PRT; 187 AA.
QBWXI5;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Collagen XVIII (Fragment).
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InterPro; IPR000024; Fz domain.
InterPro; IPR001791; Laminin_G.
InterPro; IPR001191; Laminin_G.
InterPro; IPR003129; TSP N.
Pfam; PF01391; COllagen; 8.
Pfam; PF06482; Endostatin; 1.
Pfam; PF06482; Endostatin; 1.
Pfam; PF01392; Fz; 1.
ProDom; PF00210; TSP N; 1.
SWART; SW00063; FRI; 1.
SWART; SW00210; TSPN; 1.
SWART; SW00210; TSPN; 1.
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Best Local Similarity 100.
Matches 13; Conservative
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920
1042
1065
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Q8WXI5
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Gaps
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1-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Multi-functional protein MFP.
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Pred. No. 0.0062;
1; Mismatches 0; Indels
                                                                                                                                                                                           Length 187;
                                                                                                                                                                                                                                                                                      0; Indels
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Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF202883, AAM52249.1; -.
InterPro; IPR010515; Endostatin.
InterPro; IPR00001; Kringle.
Pfan; PF06482; Endostatin; 1.
ProDom; PD000395; Kringle; 1.
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Strausberg R.;
Strausberg R.;
Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC033115; AAH33715.1; ---
HSSP; P39060; IBNL.
Collagen.
NON TER 1 1
SEQUENCE 187 AA; 20448 MW; 72B1047DB5838CD3 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Similar to collagen, type XVIII, alpha 1 (Fragment)
                                                                                                                                                                                      Score 62; DB 2;
Pred. No. 0.0043;
1; Mismatches (
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GO; GO:0006817; P:phosphate transport; IEA.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008160; Collagen.
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92.3%;
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Best Local Similarity 92.39,
The state of the
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                                                                                                                                                                                                                                        Best Local Similarity 92.3
Matches 12; Conservative
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SEQUENCE FROM N.A.
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MEDLINE-99411346; PubMed-9738008; DOI=10.1074/jbc.273.39.25404;
Halfter W., Dong S., Schurer B., Cole G.J.;
"Collagen XVIII is a basement membrane heparan sulfate proteoglycan.";
J. Biol. Chem. 273:25404-25412(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=2028799; PubMed=10830953; DOI=10.1038/35012518; Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
                                                 Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND VARIANT ILE-841.
MEDILTE=88146096; PubMed=9503385; Dol=10.1016/S0945-053X(98) 90003-8; MEDILTE=98146096; PubMed=9503385; Dol=10.1016/S0945-053X(98) 90003-8; Saarela J. Ylikarppa R., Rehn M., Purmonen S., Pihlajaniemi T.; Complete primary structure of two variant forms of human type XVIII collagen and tissue-specific differences in the expression of the Matrix Biol. 16:19-228 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAIH HUMAN STANDARD; PRT; 1516 AA.
P39060; Q9UK38; Q9Y6Q7; Q9Y6Q8;
01-FEB-1995 [Rel. 31, Created)
29-MR-2004 (Rel. 34, Last sequence update)
25-OKT-2004 (Rel. 45, Last annotation update)
Collagen alpha 1(XVIII) chain precursor [Contains: Endostatin].
Name=COL18A1;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SEQUENCE 1344 AA; 137402 MW; 7AA366E4FE940CCD CRC64;
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                                                                                                                                                                                                                                                                                                                                                             Halfter W., Dong S.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF083440; AAC33294.2;
HSSP: P39660; 1BNL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005138; F:structural molecule activity; IEA.
GO; GO:0005139; P:cell adhesion; IEA.
GO; GO:0006117; P:phosphate transport; IEA.
InterPro; IPR008161; Clg_helix.
InterPro; IPR008161; Collagen.
InterPro; IPR008185; ConA_like_lec_gl.
InterPro; IPR001319; Endostatin.
InterPro; IPR001319; TSPN.
Fam; PF06482; Endostatin; 1.
ProDom; PR001001; Collagen; 8.
Pfam; PF06482; Endostatin; 1.
ProDom; PR001001; Clg_helix; 3.
SWART; SW00210; TSPN; 1.
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1167 QPALHLVALNTPL 1179
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                           Gallus gallus (Chicken).
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es 12; Conserv
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                     Gallus.
NCBI_TaxID=9031;
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1D CAAHH HA
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DT 26-VARR

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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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92.3%; Pred. No. 0.034;
iive 1; Mismatches 0; Indels
                                                                                                                                                                                                        93.9%; Score 62; DB 2; Length 816; 92.3%; Pred. No. 0.02;
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                                                                                                                           NON TËR 1 1
SEQÜENCE 816 AA; 82553 MW; 5D539B2946694F86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Type XVIII collagen short variant. Homo eaplens (Human).
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Last annotation update)
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InterPro; IPR010515; Endostatin.
                   Pfam; PP01391; Collagen; 5.
Pfam; PF06482; Endostatin; 1.
ProDom; PD000007; Clg_helix; 2.
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SMART; SM00210; TSPN; 1.
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(TrEMBLrel. 18, I
(TrEMBLrel. 26, I
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nes 12; Conservative
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01-OCT-2001 (
01-MAR-2004 (
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SEQUENCE
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RESULT 8
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RESULT 9 093419 ID 0934: AC 0934: DT 01-00 DT 01-00

Matches

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Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Aakawa S.,
Shintani A., Sasaki T., Magamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
The DNA sequence of human chromosome 21.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=Short; Synonyms=NGI-303;
IsoId=P39060-2; Sequence=VSP_001155, VSP_001156;
IsoId=P39060-2; Sequence=VSP_001155, VSP_001156;
In liver, lung and kidney.
-!- PTM: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are hydroxylated in some or all of the chains.
-!- POLYMORPHISM: There is an association between a polymorphism in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANTS LEU-49; ARG-111; ILE-841 AND ARG-886, AND CHARACTERIZATION OF VARIANT ASN-1437.

VARIANT ASN-1437.

PubMed=14695535; DOI=10.1002/humu.10284;
Menzel O., Bekkeheien R.C.J., Reymond A., Fukai N., Boye E., Kosztolanyi G., Aftimos S., Deutsch S., Scott H.S., Olsen B.R., Antonarakis S.E., Guipponi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INVOLVEMENT IN KNOBLOCH SYNDROME.
MEDLINE=20400145; PubMed=1094434; DOI=10.1093/hmg/9.13.2051;
MEDLINE=20400145; PubMed=1094434; DOI=10.1093/hmg/9.13.2051;
Passoos-Bueno M.E.;
"Collagen XVIII, containing an endogenous inhibitor of angiogenesis and tumor growth, plays a critical role in the maintenance of retinal structure and in neural tube closure.";
Hum. Mol. Genet. 9:2051-2058(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARIANTS ILE-841 AND ASN-1437.
MEDLINE=21518361; PubMed=11666364;
Iughetti P., Suzuki O., Godoi P.H., Alves V.A., Sertie A.L.,
Zorick T., Soares F., Camargo A.A., Moreira E.S., di Loreto C.,
Moreira-Filho C.A., Simpson A., Oliva G., Passos-Bueno M.R.;
"A polymorphism in endostatin, an angiogenesis inhibitor, predisposes for the development of prostatic adenocarcinoma.";
Cancer Res. 61:7375-7378(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Knobloch syndrome: novel mutations in COL18A1, evidence for genetic heterogeneity, and a functionally impaired polymorphism in
                                                                                                                                                                                                                                                                          SEQUENCE OF 834-1516 FROM N.A., AND VARIANT ARG-886.
MEDLINE=94245237; PubMed=8188291;
Oh S.P., Warman M.L., Seldin M.F., Cheng S., Knoll J.H., Timmons S.,
Olsen B.R.;
                                                                                                                                                                                                                                                                                                                                                                  "Cloning of cDNA and genomic DNA encoding human type XVIII collagen and localization of the alpha 1(XVIII) collagen gene to mouse chromosome 10 and human chromosome 21."; Genomics 19:494-499(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endostatin.";

Hum. Mutat. 23:77-84(2004).

-!- FUNCTION: COLAIRA probably plays a major role in determining the retinal structure as well as in the closure of the neural tube.

-!- FUNCTION: Endostatin potently inhibits endothelial cell proliferation and angiogenesis. May inhibit angiogenesis by binding to the heparan sulfate proteoglycans involved in growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhi-Yong H., Biao L., Wei-Jie Z., Xiang-Fu W.; "Cloning and expression of human endostatin gene in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=2;
Name=Long; Synonyms=NC-493;
IsoId=P39060-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1334-1516 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   factor signaling.
ALTERNATIVE PRODUCTS:
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
position 1437 and prostate cancer. Heterozygous Asn-1437 individuals have a 2.5 times increased chance of developing prostate cancer as compared with homosygous Asp-1437 individuals.

-!- DISEASE: Defects in COL18A1 are a cause of Knobloch syndrome (KNO) [MIN:26750]; an autosomal recessive disorder defined by the occurrence of high myopia, vitreoretinal degeneration with retinal detachment, macular abnormalities and occipital encephalocele.
-!- SIMILARITY: Belongs to the fibril-associated collagens with interrupted helices (FACIT) family.
-!- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIM, 267750, -.

MIM, 2670002881; C:collagen; TAS.

GO; GO:0009887; P:organogenesis; TAS.

GO; GO:0007601; P:visual perception; TAS.

InterPro; IPR008161; Clalagen.

InterPro; IPR008965; ConA like lec_gl.

InterPro; IPR001791; Laminin G.

InterPro; IPR0013129; TSPN.

Pfam; PF01391; Collagen; S.

Pfam; PF01391; Collagen; S.
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Collagen alpha 1(XVIII) chain.
Endoctatin.
TSP N-terminal.
Nonhelical region 1 (NC1).
Triple-helical region 2 (NC2).
Triple-helical region 3 (NC3).
Triple-helical region 3 (NC3).
Triple-helical region 4 (NC2).
Triple-helical region 5 (NC2).
Triple-helical region 7 (NC1).
Nonhelical region 6 (NC6).
Triple-helical region 6 (NC6).
Triple-helical region 7 (NC7).
Triple-helical region 6 (NC6).
Triple-helical region 6 (NC6).
Triple-helical region 9 (COL6).
Nonhelical region 9 (NC9).
Triple-helical region 9 (NC9).
Triple-helical region 9 (NC9).
Triple-helical region 9 (NC1).
Triple-helical region 9 (NC1).
Triple-helical region 10 (NC10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure; Alternative splicing; Cell adhesion; Collagen;
Extracellular matrix; Glycoprotein; Hydroxylation; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nombelical region II (NCII).
N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                   EMBL; L22548; AAA51864.1; -.
EMBL; AF184060; AAF01310.1; ALT INIT.
PDB; 1BNL; X-ray; A/B/C/D=1334-1511.
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Pfam; PF02210; TSP N; 1.
ProDom; PD000007; Člg_helix; 1.
SMART; SM00210; TSPN; 1.
                                                                                                                                                                                                                                                                                                    EMBL; AF018081; AAC39658.1; -.
EMBL; AF018082; AAC39659.1; -.
EMBL; AL163302; CAB90482.1; -.
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Genew, HGNC:2195; COL18A1.
MIM; 120328; -.
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SIGNAL 1
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MEDLINE=22980396; PubMed=14614989; DOI=10.1016/S0945-053X(03)00073-8;
Blanma H., Shellman A., Rehn M., Autio-Harmainen H., Pihlajaniemi T.;
"Characterization of the human type XVIII collagen gene and
proteolytic processing and tissue location of the variant containing a frizzled motif.";
                                                                                                                                                                                                                                                                                                                                                                               Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                    Score 62; DB 2; Length 1516; Pred. No. 0.039;
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Remai, AY484969; AAR83296.1; JOINED.

Remai, AY484969; AAR83296.1; JOINED.

EMBL; AY484970; AAR83296.1; JOINED.

EMBL; AY484971; AAR83296.1; JOINED.

Remai, Remai, Remain, Lea, Collagen.

Remai, Remai, Remolosts; Endostatin.

Remai, PRO1391; Collagen.

Remai, PRO1391; Director.

Remain PRO1391; Director.
                                                                                                                                                                                                                                 1516 AA; 153779 MW; 38D0F23D3FD758A4 CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Type XVIII collagen long variant.
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Pred. No. 0.045;
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                                                Pfam; PP06121; DUP959; 1.
Pfam; PP06488; Bndostatin; 1.
ProDom; PD000007; Clg helix; 1.
SMART; SM00210; TSPN; 1.
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SMART; SM00063; FRI; 1.
SMART; SM00210; TSPN; 1.
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Pfam; PF01392; Fz; 1.
ProDom; PD000007; Clg_helix; 1
                                                                                                                                                                                                                                                                                                    93.9%;
92.3%;
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92.3%;
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Les 12, Conservative
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                                                                                                                                                                                               Collagen.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collagen.
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q6RZ40
Q6RZ40;
                                                                                                                                                                                                                                                                                                                                              Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
Q6RZ40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
               ઠ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DO BRANK REPARENT OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ઠે
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heterozygotes may cause Knobloch syndrome when in combination with a frameshift/truncating mutation).
                                                                                                                                                                                                                                                                                                                                                                            -> MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=22980396; PubMed=14614989; DOI=10.1016/S0945-053X(03)00073-8; Blamaa H., Snellman A., Rehn M., Autio-Harmainen H., Pihlajaniemi T.; "Characterization of the human type XVIII collagen gene and proteolytic processing and tissue location of the variant containing frizzled motif.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D -> N (decreased activity for binding laminin; increased risk of developing prostate cancer; in compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Type XVIII collagen middle variant.
Homo sapiens (Human).
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                    HTTEAGTLPÄPTPSPPSLGRPWAPLTGPSVPPPSS
PRCPWPWPRRRRLLDVLAPLVLLLGVRAASAEP (1
                                                (Potential).
(Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
N-linked (GlcNAc. .) (Potential).
O-linked (GalNAc. .).
/FTId=CAR 000150.
By similarity.
By similarity.
Cell attachment site (Potential).
Missing (in isoform Short).
/FTId=VSP_001155.
               (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 1; Length 1516; Pred. No. 0.039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY484968; AAR83297.1; JOINED.
EMBL; AY484968; AAR83297.1; JOINED.
EMBL; AY484970; AAR83297.1; JOINED.
EMBL; AY484970; AAR83297.1; JOINED.
EMBL; AY484971; AAR83297.1; -INDED.
EMBL; AY484971; C:CYPOLABS.
EMBL; AY484971; AAR83297.1; -INDED.
EMBL; AY484971; AAR83297.1; AAR83297.1; AAR83297.1; -INDED.
EMBL; AY484971; AAR83297.1; AAR83297.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q -> L.
/FTId=VAR_018053.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTId=VAR_018054.
                                                                                                                                                                                                                                                                                                                                                                                                                                               isoform Short).
/FTId=VSP_001156.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTIG=VAR_018055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ? -> R. _ _ /FTId=VAR 018056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1516 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 0.03
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 OPVLHLVALNTPL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
           129
164
691
1329
                                                                                                                                                                                    1506
1498
1097
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1437
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Best Local Similarity
Matches 12; Conserv
                                                                                  691
1329
                                                                                                                                                                                       1366
1468
1095
                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     886
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                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                    DISULFID
                                                                                                                CARBOHYD
                                                                                                                                                                                                                                                                                                 VARSPLIC
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Q6RZ39 Q6RZ39

RESULT 11

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                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIMS-Sprague-Dawley;
MEDLINE=20225; Pubmd=10766159;
Perletti G., Concari P., Giardini R., Marras E., Piccinini F., Folkman J., Chen L.;
Folkman J., Chen L.;
Faltitumor activity of Endostatin against carcinogen-induced rat primary mammary tumors.";
Cancer Res 60:1793-1796(2000).
EMBL; AF189709; AAF00975.1; -
HSSP; P39061; 1DY1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  92.4%; Score 61; DB 2; Length 226; 100.0%; Pred. No. 0.0081; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                     226 AA; 25350 MW; 38B83C0486C0E949 CRC64;
                                               01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Collagen XVIII (Fragment).
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein MGC76284.
 226 AA.
                                 Created)
PRT;
                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR010515; Endostatin.
                                                                                                                                                                                                                                                                                                                                                                Pfam; PF06482; Endostatin; 1.
                               01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 PVLHLVALNTPL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SO PVLHLVALNTPL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xenopodinae; Xenopus.
NCBI_TaxID=8364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=MGC76284;
                                                                                                                                                                                                                                                                                                                                                                                                     NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     Collagen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q6P3M9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
 DDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDTTDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDDTTDDD
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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L. Feingold E.A., Grouse L.H., Derge J.G.,
RIJausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
A Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
R Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A Raha S.A., Loquellano N.A., Peters G.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Maruy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Willalon D.K., Maruy D.M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Rlakesley R.W., Touchman J.W., Gromutz J., Myers R.M., Butterfield Y.S.,
A Unisk S.J., Marra M.A.,
And mouse cDNA sequences.;
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
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                                                                                                                                                                                                                                                                                         TISSUB=EMDIYO;

Kilein S., Gerhard D.S.;

Kilein S., Gerhard D.S.;

Kilein S., Gerhard D.S.;

Kilein S., Gerhard D.S.;

Robin EMBL, BC063229; AAH6329.1; --

ROS, GO:0005737; G:cytoplasm; IEA.

ROS, GO:0005139; F:structural molecule activity; IEA.

ROS, GO:0006817; P:structural molecule activity; IEA.

ROS, GO:0006817; P:structural molecule activity; IEA.

ROS, GO:000817; P:structural molecule activity; IEA.

ROS, GO:0001519; P:structural molecule activity; IEA.

ROS, GO:000119; P:structural molecule activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lypothetical protein.
1301 Aa; 133387 MW; 238BAEEC3FAA4383 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB 2;
Pred. No. 0.05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1310 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Preα. ...
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1125 PVLHLVALNTPL 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 PVLHLVALNTPL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00210; TSPN; 1
Collagen; Hypothetical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae; Xenopus.
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGC76284 protein.
Name=MGC76284;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=8364;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Q6DFR4
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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN 121

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Kiein S., Garhard D.S.;

RD SUDMITTEE GOOF STORE STRUCTURAL MOLECULE ACTIVITY; IEA.

DR GO; GO:0005137; C:Cytoplasm; IEA.

DR GO; GO:000155; P:cell adhesion; IEA.

DR InterPro; IPR008161; Clg helix.

DR InterPro; IPR008165; Collagen.

DR InterPro; IPR0131; Collagen.

DR InterPro; IPR0131; Collagen.

DR InterPro; IPR0131; Collagen.

DR InterPro; IPR0131; Collagen.

DR Probom; PP000007; Clg_helix; 7.

DR PRART; SM00210; TSPN; 1.

DR Probom; PD000007; Clg_helix; 3.

DR SRART; SM00210; TSPN; 1.

SQ SEQUENCE 1310 AA; 134223 MW; A369B2877758B422 CRC64;

SQ SEQUENCE 1310 AA; 134223 MW; A369B2877758B422 CRC64;

Autches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 PVLHLVALNTFL 13
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Search completed: March 10, 2005, 11:09:30 Job time : 54.3421 secs

1134 PVLHLVALNTPL 1145

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GenCore version 5.1.6
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sw model - protein search, using OM protein March 10, 2005, 11:00:49; Search time 11.2895 Seconds (without alignments) 110.795 Million cell updates/sec Run on:

US-09-766-412-30 66 Title: Perfect score:

QPVLHLVALNTPL 13 Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

283416 segs, 96216763 residues Searched:

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	collagen	collagen	collagen alpha	collagen alpha	MOT1 protein -	hypothetical pr	conserved hyp						hypothetical	hypothetical	hypothetical	hypothetical	acetyl-CoA ca					transforming prote					hypothetical	
SUV	ā	A56101	B56101	A53019	A53317	822775	C70602	AH1045	D75319	140791	AB0796	G96541	T50954	E72631	T25958	T44958	T15104	T06161	GNVSPV	850397	QQBE4	A96542	TVHUSK	PNBPF6	T22264	T48425	A83534	S56374	0.500
	DB	7	~	~	~	~	7	7	~	7	8	~	N	N	~	7	~	~	-	~	7	~	ч	Н	~	7	7	ч	•
	Query Match Length	1315	1774	684	1388	1867	176	342	190	333	425	533	103	160	258	336	617	2311	3206	102	191	519	728	72	298	323	331	342	,
æ	Query Match	100.0	100.0	93.9	66.7	65.2	9.09	9.09	59.1	59.1	59.1	59.1	57.6	57.6	57.6	57.6	57.6	57.6	57.6	56.1	56.1	56.1	56.1	54.5	54.5	54.5	54.5	54.5	1
	Score	99	99	62		43	40	40	39	39	39	39	38	38	38	38	38	38	38	37	37	37	37	36	36			36	
	co i	-	8	٣	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22		24			27	oc

. מזכיית [מין יומלוכתייל	protection and the	probable glycerol	phosphate ABC tran	conserved hypothet	hypothetical prote	hypothetical prote	probable nuclear p	hypothetical prote	H+/K+-exchanging A	high-affinity pota	high-affinity pota	outer membrane lip	probable outer mem	potassium-transpor	probable glucose-i	hypothetical prote
97051	0000	H72748	G82286	AG0977	B86033	C91186	T37889	F83574	PWECCK	E85569	D90719	A81149	H81874	AE0587	H71260	B72729
r	4	~	~	~	~	N	N	N	-	N	~	~	~	~	~	7
9	ה ה	370	548	651	959	959	1162	111	190	190	190	193	193	195	222	222
4		54.5	54.5	54.5	54.5	54.5	54.5	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0	53.0
36	2	36	36	36	36	36	36	32	32	32	32	32	32	32	32	35
,	2	31	32	33	34	35;	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT 1

_	A56101
_	collagen alpha 1(XVIII) chain precursor, short splice form - mouse
_	N; Contains: endostatin
	C;Species: Mus musculus (house mouse)
	C;Date: 03-Oct-1995 #sequence revision 08-May-1998 #text change 09-Jul-2004
	C; Accession: A56101; A58371; S72450; S65595
	R; Rehn, M.; Pihlajaniemi, T.
	J. Biol. Chem. 270, 4705-4711, 1995
	A, Title: Identification of three N-terminal ends of type XVIII collagen chains and tiss
	tif homologous to rat and Drosophila frizzled proteins.
	A; Reference number: A56101; MUID:95181468; PMID:7876242
	A;Accession: A56101
	A;Molecule type: mRNA
	A;Residues: 1-103 <reh1></reh1>
	A;Cross-references: UNIPROT:P39061; GB:U11636; NID:g618427; PIDN:AAC52178.1; PID:g61842
	R; Rehn, M.; Pihlajaniemi, T.
	Proc. Natl. Acad. Sci. U.S.A. 91, 4234-4238, 1994

Aritle: Alphal (XVIII), a collagen chain with frequent interruptions in the collagenous A; Reference number: A58371; MUID:94240112; PMID:8183894
A; Reference number: A58371; MUID:94240112; PMID:8183894
A; Accession: A58371
A; Residues: 1-928 «REHZ>
A; Cross-references: GB:L16898; NID:9404754; PIDN:AAA37434:1; PID:9553894
B; Ch, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, B.R.
A; Reference number: S72450
A; Recession: S72450 A; Molecule type: mRNA , 689-734, 'F', 736-751, 'R', 753-1315 <OHW> A; Residues: 28-687, 'L', 689-734, 'F', 736-751, 'R', 753-1315 <OHW> A; Cross-references: EMBL:L22545; NID:g348968; PIDN:AAA19787.1; PID:g511298 A; Cross-references: EMBL:L22545; NID:g348968; PIDN:AAA19787.1; PID:g511298 B; OH, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R. B; Oh, C. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994 A; Title: Isolation and sequencing of CDNAs for proteins with multiple domains of Gly-Xa A; Reference number: A58370; MUID:94240111; PMID:9183893

A;Accession: S65595
A;Molecule type: mRNA
A;Cross-references: EMBL:122545
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit
lated and subsequently O-glycosylated.
C;Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in per
C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of un
ay be useful in treating solid tumors.

A,Gene: MGI:CollBal

A,Cross-references: MGI:71175
A;Map position: 10:41.0
C;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteogly.
C;Keywords: alternative splicing; predicted <SIG>
F;24-235/Domain: signal sequence #status predicted <SIG>
F;24-235/Region: thrombospondin amino-terminal homologous
F;26-1315/Product: collagen alpha 1(XVIII) chain, short splice form #status predicted <

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1597 QPVLHLVALNTPL 1609
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Best Local Similarity luv...
Best Local 13; Conservative
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A, Cross-references: MGI:71175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C, Genetics:
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A/Reterence number: A65101, MUID:95181468; PMID:7876242
A/Reterence number: A65101
A/Reterence number: A75450
A/Reterence number: A7550
A/Reterence nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nicontains: collagen alpha IIXVIII) chain precursor, medium splice form, endostatin Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cispecies: 03-0oc-1995 #sequence revision 08-May-1998 #text change 09-Jul-2004
Ciscossion: B56101; C56101; S72450; S65595; PN0675; A54072; A58816
R;Rehn, M.; Pihlajaniemi, T.
Biol. Chem. 270, 4705-4711, 1995
A;Title: Identification of three N-terminal ends of type XVIII collagen chains and tissutif homologous to rat and Drosophila frizzled proteins.
A;Reference number: A56101; MUID:95181468; PMID:7876242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         collagen alpha 1(XVIII) chain precursor, long splice form - mouse N;Contains: collagen alpha 1(XVIII) chain precursor, medium splice form; endostatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;983-1000/Domain: collagenous #status predicted <CO10>
F;1132-1315/Product: endostatin #status predicted <EST>
F;1139-1315/Region: multiplexin collagen carboxyl-terminal homologous
F;126,488/Binding site: carbobydrate (Asn) (covalent) #status predicted
F;172-28/Disulfide bonds: #status predicted
F;172-245/Disulfide bonds: #status predicted
F;240,245,1257/Binding site: carbobydrate (Ser) (covalent) #status predicted
F;451,454,594/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
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                            F364-437/Domain: collagenous #status predicted <CO2>
F364-437/Domain: collagenous #status predicted <CO3>
F607-689/Domain: collagenous #status predicted <CO3>
F704-745/Domain: collagenous #status predicted <CO5>
F759-831/Domain: collagenous #status predicted <CO5>
F842-874/Domain: collagenous #status predicted <CO5>
F842-910/Domain: collagenous #status predicted <CO5>
F892-894/Region: collagenous #status predicted <CO9>
F993-1000/Domain: collagenous #status predicted <CO9>
F983-1000/Domain: collagenous #status predicted <CO1>
F983-1000/Domain: collagenous #status predicted <CO1
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Conservative 0
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Best Local Similarity
Matches 13; Conserv
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A; Molecule type: DNA; mRNA
A; Residues: 1293-1403, 'R', 1405-1774 <REH3>
A; Residues: 1293-1403, 'R', 1405-1774 <REH3>
A; Cross-references: GB:U03114; NID:9487733; PIDN:AAA20657.1; PID:9487734
R;O'Reilly, M.S.; Boehm, T.; Shing, Y.; Fukai, N.; Vasios, G.; Lane, W.S.; Flynn, E.; Bl.
Cell 88, 277-285, 1997
A; Title: Endostatin: an endogenous inhibitor of angiogenesis and tumor growth.
A; Reference number: A58816; MUID:97160848; PMID:9008168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A. Molecule type: protein
A. Residues: 1591-1610 < ORBS
A. Residues: 1591-1610 < ORBS
A. Residues: 1591-1610 < ORBS
A. Experimental acurce: hemangioendothelium cells
A. Note: inhibits endothelial cell proliferation
C. Comment: Prolines and lysines at the third position of the tripeptide repeating unit (() tated and subsequently O-glycosylated.
C. Comment: The different splice forms of collagen alpha 1(XVIII) may be involved in perion of comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of unity be useful in treating solid tumors.
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A/TOBSTICATE 1295/3; 1310/1; 1311/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1599/
A/INTERORS: 1295/3; 1310/1; 1331/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1599/
A/INTERORS: 1295/3; 1310/1; 1331/1; 1345/3; 1388/3; 1437/1; 1461/3; 1505/3; 1516/3; 1599/
A/NOTE: the list of introng is incompletes inhibitor; chondroitin sulfate proteoglyce
C/Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteoglyce
F;1-239, 487-1774/Product: collagen alpha 1(XVIII) chain precursor, medium splice form #s;
F;1-239, 487-1774/Product collagenous #status predicted <COO3>
F;76-812/Domain: collagenous #status predicted <COO3>
F;106-1148/Domain: collagenous #status predicted <COO5>
F;106-1148/Domain: collagenous #status predicted <COO5>
F;106-1148/Domain: collagenous #status predicted <COO5>
F;1310-1233/Domain: collagenous #status predicted <COO5>
F;1310-1233/Domain: collagenous #status predicted <COO5>
F;1310-1333/Domain: collagenous #status predicted <COO6>
F;1310-1353/Pomain: collagenous #status predicted <COO6>
F;13177-1428/Domain: collagenous #status predicted <COO10>
F;1317-1428/Domain: collagenous #status predicted <COO10>
F;1317-1428/Domain: collagenous #status predicted <COO10>
F;1317-1459/Domain: collagenous #status predicted <COO10>
F;159-1-174/Forduct: endostatin #status predicted <COO10>
F;159-1-174/Forduct: endostatin #status predicted <EST>
F;151-177-147/Fyraiding site: carbohydrate (Sar) (covalent) #status predicted <EST) #status predict
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NyContains: endostatin
Cypecies: Homo sapiens (man)
Cypecies: Homo sapiens (man)
Cypecies: Howo sapiens (man)
Cypecies: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 15-Sep-2003
CyAccession: A53019
CyAccession: A53019
CyAccession: A53019
A; Hele: Cloning of CDNA and genomic DNA encoding human type XVIII collagen and localiza A; Reference number: A53019; MUID:94245237; PMID:8188291
A,Title: Primary structure of the alphal chain of mouse type XVIII collagen, partial st.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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A;Residues: 1-684 <OHA>
A;Cross-references: GB:L22548; NID:g348908; PIDN:AAA51864.1; PID:g562794
A;Note: the cited accession number, L25548, is not in Genbank release 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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                                                                                                                         A;Reference number: A54072; MUID:94245707; PMID:8188673
A;Accession: A54072
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A;Residues: 1-176 <COL>
A;Cross-references: GB:294752; GB:AL123456; NID:g3261731; PIDN:CAB08143.1; PID:g2052135
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Species: Mycobacterium tuberculosis
C; Decies: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hanlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom A;Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein Rv1000 - Mycobacterium tuberculosis (strain H37RV)
C,Species: Mycobacterium tuberculosis
C,Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: Mycobacterium tuberculosis hypothetical protein Rv1000
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637 QPILHL--LNTPV 647
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Collagen alpha 1(XV) chain precursor - human

Collagen alpha 1(XV) chain alpha 1(XV) chain

Collagen alpha 1(XV) chain captures (man)

Collagen and collagen alpha 1(XV) chain

Collagen and collagen alpha 1(XV) chain

Rivitide: Primary structure of the alpha 1 chain of human type XV collagen and exon-intron Anelegence: University 1994

Anitide: Primary structure of the alpha 1 chain of human type XV collagen and exon-intron Anelegence: University 1994

Anitide: Primary structure of the alpha 1 chain of human type XV collagen and exon-intron Anelegence: University 1990

Anitide: Collagen and conceptual translation not complete

Rivingalal Y. The Anit human alpha 1 (XV) collagen chain contains a large amino-terminal non-triple Aintearch human alpha 1 (XV) collagen chain contains a large amino-terminal non-triple Aintearch human alpha 1 (XV) collagen chain contains a large amino-terminal and Aintearch human alpha 1 (XV) collagen chain contains a large amino-terminal non-triple Aintearch human alpha 1 (XV) collagen chain contains a large amino-terminal contains a large amino-terminal contains a large amino-terminal non-triple Aintearnes (Belbalains)

Aintearch human alpha 1 (XV) collagen chain (Bib 1992)

Aintearch human alpha 1 (XV) collagen chain (Bib 1992)

Aintearch human alpha 1 (XV) collagen chain (Bib 1992)

Aintearch human alpha 1 (XV) collagen chain (Bib 1992)

Aintearch human alpha 1 (XV) collagen chain (Bib 1992)

Aintearch human alpha 1 (XV) collagen chain (Bib 1992)

Aintearch human alpha 1 (XV) chain Hataus predicted collagen chain, alpha 1 (XV) chain Retaus predicted collagen alpha 1 (XV) chain collagen carboxyl-terminal homologous
A;Note: in the authors' translation, 482-Gly is not shown, residues 483-490 are shifted C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit (lated and subsequently O-glycosylated.

C;Comment: Different splice forms of collagen alpha 1(XVIII) may be involved in perivase C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of un c;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of un c;Genetics:

C;Genetics:
A;Gene: GDB:COL18A1

A;Cross-references: GDB:138752; OMIM:120328
A;Map position: 21q22.3-21q22.3
C;Keywords: alternative splicing; angiogenesis inhibitor; chondroitin sulfate proteoglyc F;1-59/Domain: collagenous | #status predicted <COS>
F;1-59/Domain: collagenous | #status predicted <COS>
F;1-2-24/Domain: collagenous | #status predicted <COS>
F;25-278/Domain: collagenous | #status predicted <COS>
F;25-278/Domain: collagenous | #status predicted <COS>
F;25-24/Negion: collagenous | #status predicted <COS>
F;26-264/Region: multiplexin collagenous | #status predicted <EST>
F;50-684/Region: multiplexin collagenous | #status | #status
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Pred. No. 0.0017;
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genome

Gaps

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Length 1867; 0; Indels

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Score 43; DB Pred. No. 18; 2; Mismatches

65.2%; 69.2%;

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MOTI protein - yeast (Saccharomyces cerevisiae)

Althernate names: protein LPR4c; protein YPL082c

C;Alternate names: protein LPR4c; protein YPL082c

C;Species: Saccharomyces cerevisiae

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

R;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004

R;Davis, J.L; Kunisawa, R.; Thorner, J.

Mol. Cell. Biol. 12, 1879-1892, 1992

Mol. Cell. Biol. 12, 1879-1892, 1992

A;Attle: A presumbtive helicase (MOTI gene product) affects gene expression and is requi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-1867 < DAA>
A; Residues: 1-1867 < CDAV>
A; Cross-references: Universes: Unive
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                                                                                                                                                   Gaps
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A;Residues: 1-1867 <HAL>
A;Cross-references: EMBL:U41849; NID:g1147608; PID:g1147612; MIPS:YPL082c
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       Length 1388;
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C;Keywords: DNA binding; nucleus; transmembrane protein
F;700-716/Domain: transmembrane #status predicted <TML>
F;1038-1054/Domain: transmembrane #status predicted <TM2>
F;1186-1202/Domain: transmembrane #status predicted <TM3>
       DB 2;
                                                                     8.7;
Score 44; DB :
Pred. No. 8.7;
1; Mismatches
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A;Cross-references: SGD:S0006003; MIPS:YPL082c
Query Match
Best Local Similarity '66.7%;
Matches 8; Conservative
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C;Species: Clostridium magnum.
C;Species: Clostridium magnum.
C;Date: O4-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 12-Jul-2004
C;Accession: 140791
R;Kruger, N.; Oppermann, F.B.; Lorenzl, H.; Steinbuchel, A.
Bacteriol. 176, $614-3630, 1994
A;Title: Biochemical and molecular characterization of the Clostridium magnum acetoin de A;Reference number: 140789; MUID:94266715; PMID:8206840
A;Accession: 140791
A;Accession: 140791
A;Accession: Lype: DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q46143; GB:L31844; NID:g472324; PIDN:AAA21745.1; PID:g472327
C;Superfamily: pyruvate dehydrogenase, El component, beta subunit
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Salmonella enterica subsp. enterica serovar Typhi
A; Note: this species has also been called Salmonella typhi
C; Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C; Accession: AB0796
R; Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, K.P. T.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A; Atchors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A; Accession: AB0502; MUID:21534947; PMID:11677608
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: 036541
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
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                                                                                         acetoin dehydrogenase (TPP-dependent) (EC 1.....) beta chain - Clostridium magnum
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A;Cross-references: GB:AL513382; PIDN:CAD07548.1; PID:g16503540; GSPDB:GN00176
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red. No. 21;
Mismatches 3
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Pred. No. 16;
3; Mismatches
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Pred. No.
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61.5%;
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58.3%;
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
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A, Molecule type: DNA
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C;Species: Deinococcus radiodurans
C;Species: O-155399 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75319
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shan, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: D75319
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-190 **WH**
A;Residues: 1-100 **WH**
A;Genetics:
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.Species: Salmonella enterica subsp. enterica servovar Typhi
A.Note: this species has also been called Salmonella typhi
A.Note: this species has also been called Salmonella typhi
A.Note: this species has also been called Salmonella typhi
C.Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C.Accession: AH1045
B.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, F.; Connerton, P.; Cronin, A.; Davis, R.M.; Dowd, L.; White, N.; Farrar, S.; Noule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.Accession: AH1045
A.Acces
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C;Genetics:
                                                                                             Gaps
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        Length 176;
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                                                                                         2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 39; DB 2;
Pred. No. 8.7;
1; Mismatches 3
        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Genetics:
A;Gene: yjeK
C;Superfamily: conserved hypothetical protein yodO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 40; DB;
Pred. No. 11;
1; Mismatches
                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein yjeK [imported]
        Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.68;
    63.6%;
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illarity 66.7%;
Conservative
Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | |||:| |||
136 PELHLLAPETPL 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                                                                                                                                                                                              103 PVVHLTALGSP 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 PVLHLVALNTPL 13
                                                                                                                                                                     12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5 HLVALNTPL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 HIVTLNTPL 11
                                                                                                                                                                     2 PVLHLVALNTP
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Best Local Similarity
Matches 8; Conserv
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Gaps

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Indels

Length 160;

A; Gene: APE1508

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-258 «WAM>
A;Residues: 1-258 «WAM>
A;Cross-references: UNIPROT: P91543; EMBL: U808139; PIDN: AAB37912.1; GSPDB: GN00020; CESP: Zc
A;Experimental source: strain Bristol N2; clone ZC204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Mattar, S.; Souquet, M.; Henrich, H.J.; Engelhard, M. submitted to the EMBL Data Library, August 1996 A;Description: The first fully resolved primary structure of an archaeal succinate-dehy. A;Reference number: 222881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZC204.3 - Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: Caenorhabditis elegans C; Species: T25-Ctr-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C; Accession: T25958 Rramer, J. Submitted to the EMBL Data Library, December 1996 A; Description: The sequence of C. elegans cosmid ZC204. A; Reference number: Z20116 A. Accession: T25958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Natronomonas pharaonis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44958
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A;Experimental source: strain SPI /28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein [imported] - Natronomonas pharaonis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Accession: T44958
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 38; DB 2;
Pred. No. 25;
2; Mismatches
                                                                                                  Score 38; DB 2;
Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.6%; Score 38; DB 2;
80.0%; Pred. No. 19;
ative 1; Mismatches
                                                                                                                                                                                       4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Search completed: March 10, 2005, 11:10:07 Job time: 11.2895 secs
                                                                                              57.6%;
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Matches 8; Conservative
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                            PVLHLVALNTPL 13
                                                                                                                                                                                                                                                                                                                             ||||:: |: |: 56 PVLHILPLDIPI 67
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312 PLCHLVALDEP 322
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A; Introns: 5/1; 123/3; 167/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 PVLHLVALNTP 12
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Best Local Similarity
7; Conserve
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LYLVALETPL
                                                                                                  Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A, Gene: CESP: 2C204.3
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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome lof the plant Arabidopsis.
A;Accession: G96541
A;Status: preliminary
A;Accession: G96541
A;Accession: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cipperies: Neurospora crassa
Cibate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
Cipate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
Cipate: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
Cipate: 15-Jul-2000 #sequence_revision 21-July 2000
Cipate: 15-July 2000
Cipate: 15-July
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72631
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takah awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyr A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Status: preliminary
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A,Residues: 1-160 «KAW»
A,Cross-references: UNIPROT.O9YBU1; DDBJ:AP000061; NID:g5104821; PIDN:BAA80507.1; PID:d1
A,Experimental source: strain K1
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C;Species: Aeropyrum pernix
C;Date: 20-Aug.1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C;Accession: E72631
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Pred. No. 6.9;
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Pred. No. 27;
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity 58.3
Matches 7; Conservative
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70 QPVLHQLQLESP 81
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neurospora

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STRAIN=1021;
MEDLINE=21395508; PubMed=11481431; DOI=10.1073/pnas.161294698;
Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
Golding B., Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Heterogeneous distribution of TT virus of distinct genotypes in multiple tissues from infected humans.";
Virology 288:358-368(2001).
EMBL; AB060592; BAB69997.1; -.
Pfam:; PF02057; TT ORF2; 1.
SEQUENCE 249 AA; 27721 MW; B9195F046E67DCBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=21488921; PubMed=11601907; DOI=10.1006/viro.2001.1097;
Okamoto H. Nishizawa T., Takahashi M., Asabe S., Tsuda F.,
Yoshikawa A.;
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ORFNames=SMb21292;
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2; Mismatches 2; Indels
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(c) 1993 - 2005 Compugen Ltd
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Wong S.S., Tae R.H., Chen R., Yang H., Liu B.K., Wang J., Teng J.L.,
Wong S.S., Tae R.H., Chen R., Yang H., Liu B., Yuen K.Y.;
The mitochondrial genome of the thermal dimorphic fungue Penicillium
marneffei is more closely related to those of molds than yeasts.";
The marneffei is more closely related to those of molds than yeasts.";
The TATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!-CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!-SIMILARITY: Belongs to the complex I subunit 3 family.

EMBL; AX347307; AAQ54933.1; -.

GO; GO:0005139; C:mitochondrion; IEA.

GO; GO:0006137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.

Mytochondrion; NAD; Oxidored q4: 1.

Pfam; PF00507; Oxidored q4: 1.

Riverbondrion; NAD; Oxidored ceductase; Ubiquinone.

SEQUENCE 135 AA; 15488 WW; ADC5CAA7CE689A05 CRC64;
                                                                                                                                                                                                   STRAIN=16M / ATCC 23456 / Biotype 1;

STRAIN=16M / ATCC 23456 / Biotype 1;

STRAIN=20020109; DubMed=1175668B; DOI=10.1073/pnas.221575398;

BEDLINE=20020109; DubMed=1175668B; DOI=10.1073/pnas.221575398;

Delvecchio V.G., Kapatrai B., Redkar R.J., Patra G., Mujer C., Los T., Ivanova N., Anderson I., Battacharyya A., Lykidis A., Reznik G., Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goltsman E., Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J., Haselkorn R., Kyrpides N.C., Overbeek R.;

The genome sequence of the facultative intracellular pathogen Brucella melitensis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
NCBI_TaxID=37727;
                                                                                               Brucella melitensis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 2; Length 417;
Pred. No. 38;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46847 MW; 9020D5F8EBDCA75B CRC64;
         01-WAR-2002 (TrEMBLrel. 20, Last sequence update) 01-WAR-2004 (TrEMBLrel. 26, Last annotation update) Hypothetical Membrane Spanning Protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=14675758; DOI=10.1016/S0014-5793(03)01307-3;
                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:443-448 (2002).
EMBL; AE009592; AAL52753.1; -.
PIR; AF3448; AF3448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF06181; DUF989; 1.
PROSITE; PS001309; CYTOCHROME_C; UNKNOWN_1.
COMPLE proteome.
SEQUENCE 417 AA; 46847 MW; 9020D5F8EBED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.5%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADH dehydrogenase subunit 3.
                                                                             OrderedLocusNames=BMEI1572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 54.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    225 STHNNYLTLPV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                             Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SPHNSYIVLPI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Penicillium marneffei.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                   NCBI_TaxID=29459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-MP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=nad3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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"The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endosymbiont Sinozhizobium meliloti.";
Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
EMBL, AL591985; CAC49196.1; ---
PIR; D95941; D95941.
InterPro; IPR0000455; CytC_heme_BS.
InterPro; IPR0000456; CytCohrome_C.
InterPro; IPR000389; DUF989.
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=2224771; PubMed=12271122; DOI=10.1073/pnas.192319099; Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F., Read T.D., Dodson R.J., Umayam L.A., Brinkac L.M., Beanan M.J., Daugherty S.C., DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J.A., Van Aken S.E., Riedmuller S., Tettelin H., Gill S.R., White O., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The Brucella suis genome reveals fundamental similarities between
                                                                                                                                                                                                                                                                                                                                       .;
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0
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Brucellaceae, Brucella.
NCBI_TaxID=29461,
                                                                                                                                                                                                                                                                                            69.5%; Score 41; DB 2; Length 412; 54.5%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.5%; Score 41; DB 2; Length 414; 54.5%; Pred. No. 38; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                       2; Indels
                                                                                                                                                                             Pfam; PF06181; DUF989; 1.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
Complete proteome; Hypothetical protein; Plasmid.
SEQUENCE 412 AA; 46126 MW; 8088BBEDCG6F8838 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 AA; 46576 MW; 9B7273469FFD36F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     animal and plant pathogens and symbionts.";
Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002)
EMBL; AE014347; AAN29300.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    414 AA.
                                                                                                                                                                                                                                                                                                                   Pred. No. 38;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000345; Cytc_heme_BS.
InterPro; IPR009056; Cytochrome_c.
InterPro; IPR010389; DUF989.
Pfam; PP06181; DUF989; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2003 (TrEMBLrel, 23, 01-MAR-2003 (TrEMBLrel, 23, 01-MAR-2004 (TrEMBLrel, 26, Hypothetical protein.
                                                                                                                                                                                                                                                                   Ouery Match
Best Local Similarity 54...
6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         225 STHNNYLTLPV 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 STHNNYLTLPV 232
                                                                                                                                                                                                                                                                                                                                                                              1 SPHNSYIVLPI 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SPHNSYIVLPI 11
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STRAIN=1330
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Q8G2G9

RESULT 3

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Gaps

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Length 135;

DB 2; 19;

Score 40; Pred. No.

67.8%; S 100.0%;

Best Local Similarity

Query Match

417 AA.

PRT;

OBYFF0; 01-MAR-2002 (TrEMBLrel. 20, Created)

PRELIMINARY;

Q8YFF0

RESULT 4
Q8YF0
ID Q8YF1
AC Q8YF1
DT 01-M

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InterPro; IPR010389; DUF989.
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NCBI_TaxID=10454;
                                                                                                                                 408 AA;
                                                                                                          Complete proteome. SEQUENCE 408 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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059545;
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Q9J894;
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Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
Valle G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Genome analysis of Photobacterium profundum reveals the complexity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-EX96243;

PubMed=15377794;

A Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
A Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
A Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
Chillingworth T., Cronin A., Crosset B., Davis P., DeShazer D.,
A Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
A Rabbinowitesh E., Rutherford K., Sanders M., Simmonds M.,
Songsivilai S., Stevens K., Tumapa S., Vesaratchavest M.,
Mhitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
"Genomic plasticity of the causative agent of melioidosis,
T "Genomic plasticity of the causative agent of melioidosis,
Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
  Gaps
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                                                                                                                                                                                                                                                                                                                                             Burkholderia pseudomallei K96243.
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Burkholderia.
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2014 (TrEMBLrel. 27, Last annotation update)
14-pothetical protein ATU2314.
Name=ATU2314; OrderedLocusNames=PBFRA2259;
Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria, Proteobacteria, Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2; Length 299
  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               high pressure adaptations.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, CR378670; CR320645.1;
INTERPROBLED CYTC heme BS.
INTERPRO; IPR00345; CYTC heme BS.
INTERPRO; IPR099056; Cytochrome_c.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38063.1; -.
32985 MW; 5993F6250CF3C589 CRC64;
                                                                                                                                                                                                                                   25-0CT-2004 (TrEMBLrel. 28, Created)
25-0CT-2004 (TrEMBLrel. 28, Last sequence update)
25-0CT-2004 (TrEMBLrel. 28, Last annotation update)
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                                                                                                                                                                                 299 AA.
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0; Mismatches
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Pred. No.
                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                       LysR family regulatory protein.
ORFNames=BPSS0606;
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63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 63.0
7; Conservative
                                                                                                                                                                                              PRELIMINARY;
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262 APHNYYAVTPI 272
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                                                                                 26 SPHNSYI 32
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                                           SPHNSYI 7
                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=272560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                              Q63MP4
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Matches
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06LPY1
10 06LPY1
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Pyrococcus.
                                                                                                                                                                                                                    Gaps
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IJKel W.F.J., van Strien E.A., Heldens J.G.M., Broer R., Zuidema D.,
Goldbach R.M., Vlak J.M.;
Bubmitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF168823; AAF33571.1; -...
GO; GO:0004527; F:exonuclease activity; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=20036646; PubMed=10567663;
IJKel W.F., van Strien E.A., Heldens J.G., Broer R., Zuidema D.,
Goldbach R.W., Vlak J.M.;
"Sequence and organization of the spodoptera exigua multicapsid
                                                                                                                                                                                                                  ö
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Pred. No. 59;
                                                                                                                                                                Length 408;
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                                                                                                                                                                                                                  Indels
                                                                                                                    44670 MW; 2D8BC0D825F26CFE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     413 AA; 48138 MW; 1B03329CD9FB34E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spodoptera exigua nucleopolyhedrovirus.
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 24, Last annotation update)
0RF41 alkaline exonuclease.
InterPro, IPR006162; Ppantne_S.
Pfam; PF06181; DUP989; J.
PROSITE; PS00190; CYTOCHROME C; UNKNOWN 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                Score 40; DB 2;
Pred. No. 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) Hypothetical UPF004 protein PH1875. OrderedLocusNames-PH1875,
                                                                                                                                                                                                                                                                                                                                                                                                                                 413 AA
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                                                                                                                                                                                                               3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleopolyhedrovirus genome.";
J. Gen. Virol. 80:3289-3304(1999).
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                                                                                                                                                                67.8%;
54.5%;
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66.7%;
                                                                                                                                                                                      Local Similarity 54.5
les 6; Conservative
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hes 6; Conservative
                                                                                                                                                                                                                                                                                         221 SRHNNYLTLPV 231
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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232 YNSYWLPV 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
"Complete sequence and gene organization of the genome of a hyper-
thermophilic archaebacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5:55-76(1998).
-! SIMILARITY: Belongs to the UPP0004 family.
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MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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DNA Res. 9:189-197(2002).
EMBL; AP005944; BAC479373.1; -.
InterPro; IPR000345; CytC_heme_BS.
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Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00729; Elp3; 1.
TIGREAMS; TIGR01578; MiaB-like-B; 1.
TIGRPAMS; TIGR00095; UPF0004; 1.
PROSITE; PS50926; TRAM; 1.
PROSITE; PS01278; UPF0004; 1.
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Pfam; PF01938; TRAM; 1.
Pfam; PF00919; UPF0004; 1.
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OrderedLocusNames=b112708;
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Matches 7; Conservative
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134 SPRNVYFILPI 144
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Q89RQ4
              SO THE PROPERTY OF THE PROPERT
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01-JUN-2001 (TrEMBLrel. 17, Last Sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 14, 17 days embryyo head cDNA, RIKEN full-length enriched
library, clone:3200001M10 product:procollagen, type XVIII, alpha 1,
full insert sequence. (Pragment).
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STRAIN=CSTBL/60; TISSUE-Head;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=IM2 / ATCC 51768 / DSM 7523;
MEDLINE=21664397; PubMed=11792669; DJI=10.1073/pnas.241636498;
Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=Col18a1;
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBL_TaxID=10090;
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                                                                                                                                            Length 442;
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                                                                                                  48389 MW; 6882BFE598C907AE CRC64;
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Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
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Last annotation update)
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EMBL; AE00981; AAL63743.1; -.
Complete proteome. 93 AA; 9497 MW; 598864288C4EF8BF3
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                                                                                                                                        Score 40; DB 2
Pred. No. 63;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                   93 AA.
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InterPro; IPR009056; Cytochrome_c.
InterPro; IPR010389; DUF989.
Pfam; PP064B1; DUF989; 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
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01-JUN-2001 (TrEMBLrel. 17, Last seq
01-MAR-2004 (TrEMBLrel. 26, Last ann
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01-MAR-2002 (TrEMBLrel. 20, Las
01-UUN-2003 (TrEMBLrel. 24, Las
Conserved within P. aerophilum.
OrderedLocusNames=PAE1807;
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NCBI_TaxID=13773;
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77.8%;
                                                                                                                                            67.88;
                                                                                                                                                               54.5%;
                                                                                                                                                                                  6; Conservative
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                                                                                                                                            Query Match
Best Local Similarity
                                                                               Complete proteome. SEQUENCE 442 AA;
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Best Local Similarity
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1 SPHNSYIVLPI 11
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01-NOV-1999
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Q9QZD2;
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C STRAIN=C57BL/6J; TISSUB=Head;
A Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Karch H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Muramatsu M., Hayashizaki Y.,
A Muramatsu M., Hayashizaki Y.,
B. Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AK014292; BAB29249:1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANT=CS/SDL/6J; TISSUE=Head;
MEDLINE=CS/SDL/6J; TISSUE=Head;
MEDLINE=CS/SDL/6J; TISSUE=Head;
MEDLINE=CS/SDL/6J; TISSUE=Head;
MEDLINE=CS/SDL/6J; TISSUE=HOATSU N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                    the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Head;
MEDLINE-2530913; PubMed=11076861; DOI=10.1101/gr.152600;
MEDLINE-2530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibate K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yanamoto R., Matsunco H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ogawa Y., Izawa M., Ohara E., Watahiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
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MGD, MGI:88451; Coll8al.

MGD, MGI:88451; Coll8al.

GO; GO:0005604; C:basement membrane; IDA.

GO; GO:0001515; C:extracellular space; TAS.

GO; GO:0001515; P:andjogenesis; IMP.

GO; GO:0001886; P:positive regulation of apoptosis; IDA.

GO; GO:0003035; P:positive regulation of cell migration; IDA.

GO; GO:0008084; P:positive regulation of cell migration; IDA.

GO; GO:0008084; P:positive regulation of cell migration; IDA.

InterPro; IPR010515; Endostatin.
                                                                                                                                                     RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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81.8%; Pred. No. 34;
iive 0; Mismatches 2; Indels
                                                                  STRAIN=CS7BL/6J; TISSUE=Head;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
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STRAIN-CS7BL/6J; TISSUE-Head;
The FANTOM Consortium,
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Best Local Similarity 81.8
Matches 9; Conservative
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Gaps

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BMBL; AJ236873; CAB44263.1; -. InterPro; IPR010515; Endostatin.
                                                                                                                                                                                                                                                            Eukaryota; Mecazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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STRAIN=Sprague-Dawley;
STRAIN=20227226; PubMed=10766159;
Perletti G., Concari P., Giardini R., Marras B., Piccinini F.,
Folkman J., Chen L.;
"Antitumor activity of endostatin against carcinogen-induced rat
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81.8%; Pred. No. 37;
ive 0; Mismatches 2; Indels
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171 AA; 18933 MW; 81BE2EE3FC2C8E72 CRC64;
                                                                                                                                                         01-MAR-2004 (TrEMBLrel. 12, Last sequence update) Collagen type XVIII, alpha (I) chain (Fragment).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Collagen XVIII (Fragment).
                                                                                                             171 AA
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                                                                                                             PRT;
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Cancer Res. 60:1793-1796(2000).
Embr., AF189709; AAF00975.1; -.
HSSP; P39061; 1DY1.
InterPro; IPR010515; Endostatin.
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Conservative
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140 SCHNSYIVLCI 150
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nes 9; Conserv
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01-DEC-2001 (TERMELrel. 19, Created)
01-DEC-2001 (TERMELrel. 19, Last sequence update)
01-DEC-2001 (TERMELrel. 19, Last annotation update)
10-DEC-2001 (TERMELrel. 19, Last annotation update)
Long cell-linked locus protein.
Long cell-linked locus protein.
Eda mays (Maize).
Eda mays (Maize).
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
PACCAD clade; Panicoideae; Andropogoneae; Zea.
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Query Match 66.1%; Score 39; DB 2; Length 226; Best Local Similarity 81.8%; Pred. No. 49; Matches 9; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. Gratlano B.I., Stiefel V., Puigdomenech P.; Gratlano B.I., Stiefel V., Puigdomenech P.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF934465; AAL26975.1; SEQUENCE 316 AA; 34551 MW; 833126FE0DBE488B CRC64;
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                                                                                                         206 SCHNSYIVLCI 216
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Search completed: March 10, 2005, 11:09:28 Job time : 46.2895 secs

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Compugen Ltd.
GenCore version
Copyright (c) 1993 - 2005
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protein search, using sw model OM protein Run on:

US-09-766-412-29 59 1 SPHNSYIVLPI 11 Perfect score:

Scoring table: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	conserved hypothet		hypothetical prote	м	conserved hypothet	conserved hypothet	hypothetical prote	collagen alpha 1(X	collagen alpha 1(X	dipeptidyl aminope	het-c2 protein - P	hypothetical prote	protein kinase (EC	phosphatidylserine	probable transcrip	hypothetical prote	PTS system, sugar		delayed rectifier	glutaryl 7-ACA acy				protein trypsin in	gepIA protein (AF1	sugar nucleotide e	etical	DNA-directed RNA p	complement C3 prec
SUMMARIES	ID	D95941	AF3448	F71200	HHFF26	E95984	A12860	H97637	A56101	B56101	A30107	859950	D83455	T07890	F83813	H70903	F83729	AC0898	T48498	T34417	140217	T41135	T19545	C64474	G96758	A96164	AF3123	T32406	G90163	C3RT
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d	Query	69.5	69.5	67.8	66.1	66.1	66.1	66.1	66.1	66.1	65.3	64.4	64.4	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	ä	61.0	61.0	61.0	61.0	61.0
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ATPase subunit 8 -	hypothetical prote	hypothetical prote	hypothetical prote	amidinotransferase	hypothetical prote	hypothetical prote	hypothetical prote	PTS system, fructo	hypothetical prote	hypothetical prote	RING finger protei	hypothetical prote	probable protein k	probable rimI prot	hypothetical prote
T11383	F84012	T24470	C87256	S44235	T20622	E64140	T04767	G70150	T39409	T28915	S49445	E91276	T38058	A70738	H97826
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Conserved hypothetical membrane protein, paralogue of Y20848 SWb21292 [imported] - Sino. C;Species: Sinorhizobium meliloti C;Species: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004 C;Accession: D95941 R;Fihan, T.M.; Waidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernar Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing end. A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Status: preliminary

A; Note that the state of the s

A;Gene: SMb21292 A;Genome: plasmid

ö Gaps ò, 69.5%; Score 41; DB 2; Length 412; 54.5%; Pred. No. 5.9; ive 3; Mismatches 2; Indels Conservative Query Match Best Local Similarity

1 SPHNSYIVLPI 11 ઠે 셤

225 STHNNYLTLPV 235

A;Accession: AF3448 A;Status: preliminary A;Molecule type: DNA

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conserved hypothetical membrane protein, paralogue of Y21292 SMb20848 [imported] - Sino. C.Species: Sinorhizobium meliloti
C.Species: Sinorhizobium meliloti
C.Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C.Accession: E95984
R.Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. US.A. 98, 9889-9884, 2001
A;Title: The complete sequence of the 1,683-48 pSymB megaplasmid from the N2-fixing endo
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-410 «KUR»
A;Residues: 1-410 «KUR»
A;Residues: 1-410 «KUR»
A;Cross-references: UNIPROT:Q92UI9; GB:AL591985; PIDN:CAC49541.1; PID:g15141028; GSPDB:CAC45Eperimental source: strain 1021, magaplasmid pSymB
A;Experimental source: strain 1021, magaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puller, A.; Abola, P.; Ampe, F.; Barloy-Hubler, pela_D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L.; Hyman, R.W.; Jones, T. Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.; Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riwood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, T erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2333, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - Agrobacterium tumefaciens (strain Ch
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A; Accession: AI2860
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C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 410;
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54.5%;
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SLHNNYLTLPV 235
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                                 29 PHSRYVLLPL 38
   PHNSYIVLPI
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Best Local Similarity
Matches 6; Conserv
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A; Residues: 1-428 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Genome: plasmid
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R) Ingolia, T.D.; Craig, E.A.
Proc. Natl. Acad. Sci. U.S.A. 79, 2360-2364, 1982
F) Ingolia, T.D.; Craig, E.A.
F) Proc. Natl. Acad. Sci. U.S.A. 79, 2360-2364, 1982
A) Title: Four small brosophila heat shock proteins are related to each other and to mamm A) Reference number: A03909; MUID: 82248004; PMID: 6285380
A) Accession: A02220
A) Molecule type: DNA
A) Residues: 1-209 < ING>
A) Note: the authors translated the codon GAC for residue 15 as Glu, CAG for residue 22 a A) Note: the codon usage table proposed by the authors and the translation of the protein C) Comment: This small heat shock protein is related to alpha crystallin.
C) Genetics:
A) Gene: FlyBase: HSP26
                A,Cross-references: UNIPROT:O8YFFO, GB:AE008917; PIDN:AAL52753.1; PID:g17983585; GSPDB:G
A,Experimental source: strain 16M
C,Genetics
A,Gene: BMEI1572
A,Map position: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein PH1875 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Jul-2004
C;Accession: F71200
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfkuu, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. S, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A;Reference number: A71000; MUID:98344137; PMID:9679194
A;Accession: F71200
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Cross-references: GB:AP000007; NID:g3236134; PIDN:BAA30997.1; PID:g3258314
A,Experimental source: strain OT3
A,Subte: this accession replaces an interim accession for a sequence replaced by GenBank C,Genetics:
A,Gene: PH1875
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C,Species: Drosophila melanogaster
C,Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-May-2004
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A;Map position: 3L (67B)
C;Superfamily: alpha-crystallin-related small heat shock protein
C;Keywords: heat shock; stress-induced protein
                                                                                                                                                                                                                           Length 417;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.8%; Score 40; DB 1; Length 432;
63.6%; Pred. No. 9.6;
cive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 50.0%; Pred. No. 6.6; 5; Conservative 4; Mismatches 1; Indels
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                                                                                                                                                                                                                    Score 41; DB 2;
Pred. No. 5.9;
3; Mismatches 2
                                                                                                                                                                                                                    69.5%;
54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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Matches 7; Conserv
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Matches 5; Conserv
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us-09-766-412-29.rpr

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C. COMMENDER: The different splice forms of collagen alpha 1(XVIII) may be involved in per ay be useful in treating solid tumors.

C. Genetics:
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A;Molecule type: mRWA
A;Rosidues: 1-562 «REH1>
A;Cross-references: UNIPROT:Q61434; GB:U11637; NID:g618429; PIDN:AAC52179.1; PID:g61843:
A;Experimental source: splice form clone PE17.24
A;Accession: C56101
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A, Residues: 487-1146, L., 1148-1193, FF, ,1195-1210, 'R', 1212-1512, 'L', 1514-1522, 'F', 1524-1.

A; Cross-references: EMBL: L22545; NID: 9348968; PIDN: AAA19707.1; PID: 9511298

A; Cross-references: EMBL: L22545; NID: 9348968; PIDN: AAA19707.1; PID: 9511298

B; Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons, S.; Ooshima, A.; Olsen, A.B.R.

Proc. Natl. Acad. Sci. U.S.A. 91, 4229-4233, 1994

A; Title: Isolation and sequencing of cDNAs for proteins with multiple domains of Gly-Xa

A; Reference number: A58370; MUD: 94240111; PMID: 8183893

A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                          angiogenesis inhibitor; chondroitin sulfate proteogly.
                                                                                                                                                                                                                                                                                                                                                                                                           short splice form #status predicted
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C; Date: 03-Oct-1995 #sequence revision 08-May-1998 #text change 09-Jul-2004
C; Date: 03-Oct-1995 #sequence revision 08-May-1998 #text change 09-Jul-2004
C; Date: 03-Oct-1995 #sequence revision 08-May-1998 #text change 09-Jul-2004
C; Date: 03-Oct-1995 #sequence revision 08-May-1998 #text change 09-Jul-2004
C; Date: 03-Oct-1995 #sequence revision 08-May-11, 1995
J; Biol. Chem. 270, 4705-4711, 1995
J; Biol. Chem. 270, 4705-4711, 1995
J; Richie: Identification of three N-terminal ends of type XVIII collagen chains and tif homologous to rat and Drosophila frizzled proteins.
A; Reference number: A56101; MUID:95181468; PMID:7876242
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(Ser) (covalent) #status predicted
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S.; Ooshima, A.; Olsen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F:1132-1315/Product: endostatin #status predicted <EST>
F:1139-1315/Region: multiplexin collagen carboxyl-terminal homologous
F:126,488/Binding site: carbohydrate (Asn) (covalent) #status predict
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Pred. No. 51;
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A;Experimental source: splice form clones PE8.1,
R;Oh, S.P.; Kamagata, Y.; Muragaki, Y.; Timmons,
submitted to the EMBL Data Library, August 1993
A;Reference number: S72450
A;Accession: S72450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;172-228/Disulfide bonds: #status predicted F;240,245,1257/Binding site: carbohydrate (Ser) F;451,454,594/Binding site: chondroitin sulfate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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81.8%;
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Best Local Similarity 81.0
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A;Cross-references: MGI:71175
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                                                                                                                                                                                                                                                                        A, Map position: 10:41.0
C; Keywords: alternative
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Abfolto

Collagen alpha 1(XVIII) chain precutsor, short splice form - mouse

Collagen alpha 1(XVIII) chain precutsor, short splice form - mouse

Collagen alpha 1(XVIII) chain precutsor, short splice form - mouse

Cyaccesaion. Asciol, A88371, $72460; $65595

Cyaccesaion. Asciol, A88371, $72460; $65595

R;Rehn, M; Phlhajaniemi, T.

J; Biol. Chem. 270, 4705-4711, 1995

A;Title: Identification of three N-terminal ends of type XVIII collagen chains and tissu tif homologous to rat and brosophila frizzled proteins.

A;Reference number: A56101

A;Reference number: A56101

A;Residues: 1-103 - REHI>
A;Residues: UNIPROT:P99061; GB:U11636; NID:G618427; PIDN:AAC52178.1; PID:G618428

R;Rehn, M; Phlhajaniemi, T acollagen chain with frequent interruptions in the collagenous A;Reference number: A58371

A;Accession: A58371

A;Accession: A58371

A;Accession: A58371

A;Residues: 1-928 - REHI>
A;Accession: A58371

A;Residues: 1-928 - REHI>
A;Accession: A58371

A;Accession: A58370

A;Accession:
                                                                                                                                                                                                                                                                                                                         Cyace: 30-Sep-Zord Hasquence_revision 30-Sep-Zord Heart_Change 09-001-2004

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2332-328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUD:21608551; PMID:11743194

A;Reference number: A97359; MUD:21608551; PMID:11743194

A;Residues: Drah
A;Residues: Drah
A;Residues: 1-428 «KUR»
A;Cross-references: UNIPROT:Q8UD14; GB:AE007869; PIDN:AAK88057.1; PID:g15157481; GSPDB:G
A;Genetics:
A;Map position: circular chromosome
                                                                                                                                                                                                                                   _4211 [imported] - Agrobacterium tumefaciens (strain C58, Cere
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A;Molecule type: mRNA
A;Residues: 28-1315 < OHS>
A;Coss-references: EMBL:L22545
C;Comment: Prolines and lysines at the third position of the tripeptide repeating unit lated and subsequently O-glycosylated.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                    ypothetical protein AGR_C 4211 [imported] - Agrobacterium tumefaciens (str. Species: Agrobacterium tumefaciens . Species: Agrobacterium tumefaciens . Set. Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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Pred. No.
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54.5%;
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                                                    233 SLHNNYLTLPV 243
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Best Local Similarity
Matches 6; Conserv
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A;Cross-references: UNIPROT:P18962; EMBL:U10399; NID:g500689; PIDN:AAB68879.1; PID:g5006.
R;Roberts, C.J.; Pohlig, G.; Rothman, J.H.; Stevens, T.H.
Cell Biol. 108, 1363-1373, 1989
A;Title: Structure, biosynthesis, and localization of dipeptidyl aminopeptidase B, an in A;Reference number: A30107; MUID:89174971; PMID:2647766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-82,'H', 94-124,'N',126-181,'LRRLET',189-199,'N',201-365,'DFKRGKERKF',376-5'
A;Cross-references: BMBL:X15484
A;Note: the authors translated the codon ACC for residue 572 as Asn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: 8R
C;Superfamily: dipeptidyl-peptidase IV
C;Keywords: dipeptidylpeptide hydrolase; glycoprotein; transmembrane protein; yeast vacu
E;30-45/Domain: transmembrane #status predicted <TMM>
F;83.79,110,139,392,421/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Status: preliminary
Modecule type: DNA
A,Residues: 1-208 <a href="mailto:agal-a">a,Residues: 1-208 <a href="mailto:agal-a">a,Residues: 1-208 <a href="mailto:agal-a">a,Cross-references: UNIPROT:Q01494; EMBL:U05236; NID:g523337; PIDN:AAA20542.1; PID:g5233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: S59950
R; Saupe, S.; Descamps, C.; Turcq, B.; Begueret, J.
R; Saupe, S.; Descamps, C.; Turcq, B.; Begueret, J.
R; Saupe, S.; Descamps, C.; Turcq, B.; Begueret, J.
A; Title: Inactivation of the Podospora anserina vegetative incompatibility locus het-c, A; Reference number: S59950; MUID:94286551; PMID:8016091
A; Accession: S59950
                                 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Podospora anserina
Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                       submitted to the EMBL Data Library, June 1994
A;Description: The sequence of S. cerevisiae cosmid 8082.
A;Reference number: S46773
A;Accession: 846773
A;Molecule type: DNA
A;Residues: 1-818 < DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
                                 #sequence_revision 30-May-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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Pred. No. 38;
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A;Gene: SGD:DAP2; STE13; MIPS:YHR028c
A;Cross-references: SGD:S0001070; MIPS:YHR028c
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S59950
het-c2 protein - Podospora anserina
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Best Local Similarity 63.0
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PHHSFLVKPI 154
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                                                                      C; Accession: S46780; A30107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 PHNGYVDILPI
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nes 6; Conserv
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Matches
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A;Residues: 487-1512,'L',1514-1522,'F',1524-1683,'V',1685-1774 <CH2>
A;Cross-references: EMBL:L22545
A;Cross-references: EMBL:L22545
B;Abbc, N.; Muragaki, T.; Yoshiboka, H.; Inoue, H.; Ninomiya, Y.
Biochem: Biophys. Res. Commun. 196, 576-582, 1993
A;Title: Identification of a novel collagen chain represented by extensive interruptions A;Reference number: PN0675; MUD:94059075; PMID:8240330
A;Reference number: PN0675
A;Molecule type: mRNA
A;Residues: 635-1774 <ABE>
A;Residues: 635-1774 <ABE>
A;Residues: 635-1329-13335, 1994
A;Rehn, M. Hintikka, E;Phlajaniemi, T.
J. Biol. Chem. 269, 13329-13335, 1994
A;Title: Primary structure of the alphal chain of mouse type XVIII collagen, partial str
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C;Comment: The different splice fores of collagen alpha 1(XVIII) may be involved in peri C;Comment: Endostatin is released from collagen alpha 1(XVIII) chain by the action of un by be useful in treating solid tumors.
C;Genetics:
A;Gene: MGI:Coll8al
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A Map position: 10:41.0
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A Introns: 10:41.0
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A; Molecule type: DNA; mRNA
A; Cross-references: GB:U03714; NID:9487733; PIDN:AAA20657.1; PID:9487734
B; O'Reilly, M.S.; Boehm, T.; Shing, Y.; Fukai, N.; Vasios, G.; Lane, W.S.; Flynn, E.; Cell 89, 277-285; 1997
A; Title: Endostatin: an endogenous inhibitor of angiogenesis and tumor growth.
A; Reference number: A58816; MUID:97160848; PMID:9008168
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F/106-1149/Domain: collagenous #status predicted <CCO3-
F/1163-1204/Domain: collagenous #status predicted <CCO6-
F/1163-1204/Domain: collagenous #status predicted <CCO6-
F/1301-1333/Domain: collagenous #status predicted <CCO6-
F/1351-1353/Pomain: collagenous #status predicted <CCO0-
F/137-1428/Domain: collagenous #status predicted <CCO0-
F/137-1429/Domain: collagenous #status predicted <CCO0-
F/142-1459/Domain: collagenous #status predicted <CCO0-
F/142-1459/Domain: collagenous #status predicted <CCO0-
F/1591-1774/Region: multiplexin collagen carboxyl-terminal homologous
F/1591-1774/Region: multiplexin collagen carboxyl-terminal homologous
F/1591-1774/Binding site: carbohydrate (Ser) (covalent) #status predicted
F/910,913,1053/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted
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Pred. No. 72;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    collagen chain.
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M.J.; B1 K.; Lim,

P.; Hickey, A.; Larbig,

C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004 C;Accession: D83455 R;Stover, C:K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hic} Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lari, i. Lory, S.; Olson, M.V.

dipeptidyl aminopeptidase B (EC 3.4.14.-) - yeast (Saccharomyces cerevisiae) N;Alternate names: protein YHR028c C;Species: Saccharomyces cerevisiae

g ð

RESULT 10

D83455 hypothetical protein PA1513 [imported] - Pseudomonas aeruginosa

RESULT 12

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Search completed: March 10, 2005, 11:10:07 Job time : 10.5526 secs
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                     Aritle: Complete genome sequence of Peeudomonas aeruginosa PA01, an opportunistic pathd Areference number: A82950; MUID:20437337; PMID:10984043
A; Reference number: A82950; MUID:20437337; PMID:10984043
A; Reference: DR3455
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-425 < STO>
A; Cross-references: UNIPROT:Q913K0; GB:AE004580; GB:AE004091; NID:g9947468; PIDN:AAG0490
C; Genetics: strain PA01
A; Gene: PA1513
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-102 <ZHA>
A;Cross-references: UNIPROT:049991; EMBL:U89682; NID:g2735253; PIDN:AAB93863.1; PID:g273
A;Experimental source: cultivar Rutgers; seedling
C;Genetics:
A;Genetics:
C;Superfamily: protein kinase homology
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F83813
A;Status: preliminary
A;Molecule type: DNA
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A;Cross-references: UNIPROT:Q9KDA4; GB:AP001511; GB:BA00004; NID:g10173727; PIDN:BAB05d
A;Experimental source: strain C-125
C;Genetics:
A;Gene: pssA
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R;Zhang, S.; Diener, T.O.
submitted to the EMBL Data Library, February 1997
A;Description: Isolation and characterization of seven serine/threonine protein kinase-e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               phosphatidylserine synthase pssA [imported] - Bacillus halodurans (strain C-125) C;Species: Bacillus halodurans C;Date: 01-Dec_2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
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C;Species: Lycopersicon esculentum (tomato)
C;Date: 14-May.1999 #sequence_revision 14-May-1999 #text_change 16-Aug-2004
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Pred. No. 23;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 54.5%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              221 SRHNNYFTLPV 231
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45 TPRNSYCAMPI 55
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Nature 406, 959-964, 2000
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Ricole, S.T.; Broach, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, Comnor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998

A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A.Authors: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A.Reteunce number: A70500; MUID:98295987; PMID:9634230

A.Accession: H70903

A.Accession: Preliminary; nucleic acid sequence not shown; translation not shown
A.Residues: 1-264 <COL>
A.Residues: 1-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable transcription regulator Rv0165c - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis (C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999 C;Accession: H70903
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Pred. No. 21;
3; Mismatches 2; Indels
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50.0%;
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Best Local Similarity 50.0
Matches 5; Conservative
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                                                                                 129 HNSFIGLPI 137
HNSYIVLPI 11
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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March 10, 2005, 11:07:00 ; Search time 66.8684 Seconds (without alignments) 54.260 Million cell updates/sec
                                                                                                                                                                                                                                    1396920 seqs, 329844858 residues
OM protein - protein search, using sw model
                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                     US-09-766-412-29
59
                                                                                                                                          1 SPHNSYIVLPI 11
                                                                                                        Title:
Perfect score:
                                                                                                                                                                               Scoring table:
                                                                                                                                            Sequence:
                                                                                                                                                                                                                                    Searched:
                                 Run on:
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1396920 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 200000000

Published Applications AA:*

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11: /cgn2_6/ptodate/2/pubpaa/US09_NEW PUB.pep:*
13: /cgn2_6/ptodate/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodate/2/pubpaa/US10A_PUBCOMB.pep:*
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19: /cgn2_6/ptodate/2/pubpaa/US60_NEW_PUB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

	Description	Sequence 29, Appl	Sequence 48112, A	Sequence 46, Appl	Sequence 18, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 3451, Ap	Sequence 8451, Ap	Sequence 2, Appli	Sequence 3, Appli	Sequence 71, Appl	Sequence 4956, Ap
	QI	US-09-766-412-29	US-10-282-122A-48112	US-10-131-241-46	US-10-292-418-18	US-10-920-820-13	US-09-998-831-13	US-10-373-561-13	US-10-128-714-3451	US-10-128-714-8451	US-09-373-938-2	US-10-080-797-3	US-10-422-934-71	US-09-815-242-4956
	DB	6	15	14	14	17	σ	14	14	14	σ	13	14	σ
	Query Match Length DB	11	638	184	184	184	191	191	201	201	207	207	207	455
æ	Query Match	100.0	67.8	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1	66.1
	Score	59	40	39	39	39	39	39	39	39	39	39	39	39
	Result No.	7	7	m	4	2	9	7	æ	σ	10	11	12	13

RESULT 2
US-10-282-122A-48112
; Sequence 48112, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

Seguence 72515, A	6	42	'n	'n	'n	'n	22(	2805	38,	25599	2446	492		514	585		1140	61727,		64349,	62628,	18	16	7	Sequence 4, Appli	ý	ω̈́	73	53	22	Sequence 13774, A
US-10-282-122A-72515	242-1077	-10-282-122A	-10 - 401 - 437	US-10-402-312-3	10-402-06	10-401-43	US-10-369-493-22029	10-424-599-2	US-10-767-701-38716	US-10-424-599-255994	0-424-599-2	0-282-12	99-2	0-425-114-5	0-767-701-5	US-10-424-599-143691	0-437-963-1	0-282-122A-	-10-282-122A-	122A-	0-282-122A-6262	10-437-96	10-240-14	-10-385-136	흠	-10-385-136	US-10-385-136-8	0-282-122A-	-10-282-122A-5961	S-10-282-122A-	US-09-815-242-13774
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66.1	66.1	66.1	65.3	65.3	65.3	65.3	65.3	64.4	64.4	64.4	64.4	64.4	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	62.7	ä	62.7	62.7
39	39	e	₩.	Θ.	8	38.5	8	38	38	38	38	38	37	37	37	37	37	37		37	37	37	37	37	37	37	37	37	37	37	37
14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

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Sequence 11. Application US/09766412

Patent No. US2002010312941

GENERAL INFORMATION:
APPLICANT: GENERAL INFORMATION:
TITLE OF INVENTION: ACTIVITY
FILE REPERENCE: 1781-0215P
CURRENT APPLICATION NUMBER: US/09/766,412

CURRENT PILING DATE: 2001-01-11

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 29

SEQ ID NO 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature;
CTHER INFORMATION: Endo-1
US-09-766-412-29
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                                                                                                                                                                                                                                                                                                                   ORGANISM: Mammalian
RESULT 1
US-09-766-412-29
                                                                                                                                                                                                                                                                                                TYPE: PRT
                                                                                                                                                                                                                                                                                                                                         FEATURE:
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Sequence 13, Application US/10920820
Publication No. US20050009144A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING DISORDERS
TITLE OF INVENTION: INVOLVING ANGIOGENESIS
TITLE OF INTENTION INVENTION: INVOLVING ANGIOGENESIS
CURRENT APPLICATION NUMBER: US/10/920, 820
CURRENT FILING DATE: 2001-08-24
PRIOR FILING DATE: 2001-08-24
PRIOR PLING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.2
                                                                                                                                                                           ó
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: 11, Yue
APPLICANT: 11, Yue
APPLICANT: Gillies, Stephen D
TITLE OF INVENTION: Expression and Export of Angiogenesis Inhibitors as
TITLE OF INVENTION: Immunofusins
FILE REFERENCE: LEX-006C1
CURRENT APPLICATION NUMBER: US/10/292,418
CURRENT FILING DATE: 2002-11-12
                                                                                                                                                                             Gaps
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                                                                                                                                   Score 39; DB 14; Length 184;
Pred. No. 65;
0; Mismatches 2; Indels
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT FILING DATE: 2002-11-12
PRIOR APPLICATION NUMBER: 09/383,315
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: US 60/097,883
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 54
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/10292418; Publication No. US20030139365A1; GENERAL INFORMATION:
SOFTWARE: PatentIn version 3.1 SEQ ID NO 46
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81.8%;
                                                                                                                Ouery Match
Best Local Similarity 81.8
---- 9; Conservative
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Best Local Similarity 81.8
Matches 9, Conservative
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                                                                                                                                                                                                               1 SPHNSYIVLPI 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Mus musculus
US-10-292-418-18
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lo, Kin-Ming
                                                                                                                                                                                                                                             164 SCHNSYIVLCI
                                                        ; TYPE: PRT
; ORGANISM: Murinae sp.
US-10-131-241-46
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US-10-920-820-13
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US-10-920-820-13
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LENGTH: 184
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LENGTH: 184
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APPLICANT: Fortier, Anne H.
APPLICANT: Fortier, Anne H.
APPLICANT: Fortier, Anne H.
APPLICANT: Fortier, Anne H.
APPLICANT: Compositions and Methods for Inhibiting Endothelial Cell Prolifer
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
TITLE OF INVENTION: and Regulating Angiogenesis Using Cancer Markers
CURRENT APPLICATION WHERE: US/10/131,241
CURRENT APPLICATION WHERE: US 09/413,049
PRIOR FILING DATE: 1999-10-06
PRIOR FILING DATE: 1999-0-21
PRIOR APPLICATION WHERE: US 09/316,802
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR APPLICATION NUMBER: US 60/086,586
PRIOR FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 65
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 46, Application US/10131241 Publication No. US20030012792A1 GENERAL INFORMATION:
            Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Burkholderia cepacia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 63.6%;
Matches 7; Conservative
                                                                                                        Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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151 TPHLSHLVLPI 161
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138 PHHSFVVKPI 147
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Publication No. US20030175276A1

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF

PILE REPERENCE: 1001.02582

CURRENT APPLICATION NUMBER: US/10/373,561

PRIOR FILING DATE: 2003-02-24

PRIOR PELICATION NUMBER: US/09/561,499

PRIOR PELICATION NUMBER: US/09/561,499

PRIOR PELICATION NUMBER: 60/131,432

PRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SEQ ID NO 13

LENGTH: 191

LENGTH: 191

LENGTH: 191

LENGTH: 191
                                                                                                                                                                                                                          Sequence 13, Application US/0999831

Patent No. US20020119153A1

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: INHIBITING VEGF

TITLE OF INVENTION: INHIBITING VEGF

FILE REFERENCE: 4001.00294

CURRENT APPLICATION NUMBER: US/09/998,831

CURRENT APPLICATION NUMBER: US/09/998,831

PRIOR APPLICATION NUMBER: 09/561,108

PRIOR PLING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 13

LENGTH: 191
                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-998-831-13
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DB 17; Length 184;
65;
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Pred. No. 68;
0; Mismatches 2; Indels
                                           Indels
                    Pred. No. 65;
0; Mismatches
  Score 39;
66.1%;
81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative (
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                  Best Local Similarity 81.8
Matches 9, Conservative
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                                                                                                                             164 SCHNSYIVLCI 174
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                                                                                    1 SPHNSYIVLPI 11
                                                                                                                                                                                                                   US-09-998-831-13
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Query Match
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1 SPHNSYIVLPI 11

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APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Tishkoff, Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
FILE REFERENCE: 10182-018-99
FILE REFERENCE: 10182-018-99
FILE REFERENCE: 2001-04-23
FRIOR APPLICATION NUMBER: US 60/287,066
FRIOR APPLICATION NUMBER: US 60/287,066
FRIOR APPLICATION NUMBER: US 60/287,066
FRIOR APPLICATION NUMBER: US 60/303,899
FRIOR PILING DATE: 2001-07-09
FRIOR APPLICATION NUMBER: US 60/316,362
FRIOR FILING DATE: 2001-07-09
FRIOR FILING DATE: 2001-07-09
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
FRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
FRIOR FILING DATE: 2001-08-31
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APPLICANT: Tishkoff Daniel
APPLICANT: Tishkoff Daniel
APPLICANT: Tishkoff Daniel
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Zamudio, Carlos
APPLICANT: Lemieux, Sebastien M
TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
TITLE OF INVENTION: Methods of Use
FILE REFERENCE: 10182-018-99
CURRENT FAPLICATION NUMBER: US/10/128,714
CURRENT FILING DATE: 2001-04-23
PRIOR APPLICATION NUMBER: US 60/285,697
PRIOR APPLICATION NUMBER: US 60/287,066
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-04-27
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-06-05
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-07-09
PRIOR FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 8603
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Pred. No. 72;
3; Mismatches 1; Indels
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; Sequence 8451, Application US/10128714
; Publication No. US20030119013A1
; GRNBRAL INFORMATION:
; APPLICANT: Jiang, Bo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; окGANISM: Aspergillus fumigatus
US-10-128-714-3451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 66.1%;
Best Local Similarity 60.0%;
Matches 6; Conservative
Sequence 3451, Application US/1
Publication No. US20030119013A
GENERAL INFORMATION:
APPLICANT: Jiang, Bo
```

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APPLICANT: Kadan, Michael
APPLICANT: Kadan, Michael
APPLICANT: Beerli, Roger
TITLE OF INVENTION: LIGAND ACTIVATED TRANSCRIPTIONAL REGULATOR PROTEINS
FILE REFERENCE: 22908-1227C
CURRENT APPLICATION NUMBER: US/10/422,934
CURRENT PILING DATE: 2003-04-23
PRIOR APPLICATION NUMBER: 09/586,625
PRIOR PILING DATE: 2000-06-02
PRIOR PILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 92
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 71
LENGTH: 207
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Pred. No. 74;
0; Mismatches 2; Indels
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APPLICANT: Aparthese, Kari L.
APPLICANT: Wall, Daniel
APPLICANT: Tradical Judith W.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: Tradick, John D.
APPLICANT: An Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
CURRENT APPLICANTON NUMBER: 60/29/815,242
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR PLILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2000-11-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: PRESED FOR WINDOWS VETSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-815-242-4956
; Sequence 4956, Application US/09815242
; Patent No. US20020061569A1
; GRNERAL INFORMATION:
APPLICANT: Hagelbeck, Robert
                                                               Sequence 71, Application US/10422934; Publication No. US20030186841A1; GENERAL INFORMATION: APPLICANT: Barbas, Carlos F., III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 66.1
Best Local Similarity 81.8
Matches 9; Conservative
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SEQ ID NO 4956
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Publication No. US20020115202A1

GENERAL INFORMATION:

BAPLICANT: Hallenbeck, Paul

APPLICANT: Hallenbeck, Paul

APPLICANT: Chen, Cheauyun Theresa

TITLE OF INVENTION: ADENOVIRAL VECTORS INCLUDING DNA SEQUENCES ENCODING ANGIOGENIC IN
FILE REFERENCE: 4-3089991

CURRENT FILIAND DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin version 3.1
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Pred. No. 72;
3; Mismatches 1; Indels
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Pred. No. 74;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/10080797
Publication No. US20020183253A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Campochiaro, Peter A.
APPLICANT: Dixon, Katharine H.
APPLICANT: Brazzell, Romulus K.
TITLE OF INVENTION: METHOD FOR TREATING OCULAR
TITLE OF INVENTION: NEOVASCULARIZATION
FILE REFERENCE: 4-31881A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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CURRENT FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 207
                                                               TYPE: PRT (CRANISM: Aspergillus fumigatus US-10-128-714-845)
                                                                                                                                                         66.1%;
60.0%;
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81.8%;
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81.8%;
SOFTWARE: PatentIn version 3.1
                                                                                                                                                         Query Match 66.1
Best Local Similarity 60.0
Matches 6; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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187 SCHNSYIVLCI 197
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138 PHHSFVVKPI 147
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                                                                                                                                                                                                                                                   2 PHNSYIVLPI 11
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US-09-373-938-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 9; Conserv
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US-10-080-797-3
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LENGTH: 207
TYPE: PRT
                     SEQ ID NO 8451
LENGTH: 201
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US-10-080-797-3
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SOFTWARE: Fast:
SEQ ID NO 10778
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CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PILING DATE: 2000-05-66

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-09

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-16

PRIOR PILING DATE: 2001-02-06

PRIOR PILING DATE: 2001-02-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Yanamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
                                                                                                            Gaps
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                                 Length 455;
Score 39; DB 9; Lengtn 400, Pred, No. 1.78+02;
                                                                                                                                                                                                                                                                                                                                                    RESULT 14
US-10-282-122A-72515
; Sequence 72515, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
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US-10-282-122A-72515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
                                 Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
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Carr, Grant
Yamamoto, Robert
Forsyth, R.
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Best Local Similarity 45.5
Matches 5; Conservative
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418 APHGGFLVLPV 428
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421 APHGGFLVLPV 431
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US-09-815-242-10778
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## APPLICANY: Haselbeck, Robert

## APPLICANY: Oblsen, Kobert

## APPLICANY: Oblsen, Kobert

## APPLICANY: Oblsen, Kari L.

## APPLICANY: Variand.

## APPLICANY: Variand.

## APPLICANY: Trawick, John D.

## APPLICANY: Trawick, John D.

## APPLICANY: Wall, Howard

## CURRENT APPLICANION INTER: 1001-03-11

## RIOR PELLING DATE: 2000-03-21

## RIOR PELLING DATE: 2000-05-23

## RIOR APPLICANION NUMBER: 60/24,578

## RIOR APPLICANION NUMBER: 60/24,578

## RIOR APPLICANION NUMBER: 60/257,931

## RIOR PELLING DATE: 2000-11-27

## RIOR PELING DATE: 2000-11-27

## RIOR PELLING DATE: 2000-10-21-27

## RIO
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Search completed: March 10, 2005, 11:15:26 Job time : 67.8684 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 10, 2005, 11:04:09 ; Search time 22.2895 Seconds (without alignments) 36.840 Million cell updates/sec Run on:

US-09-766-412-29 59

1 SPHNSYIVLPI 11 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

513545 segs, 74649064 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Issued Patents AA: Database :

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		de			SUMMAKIES	
Result No.	Score	Query Match	Query Match Length	DB	ID	Description
1	59	100.0	1	m	US-09-385-442-29	Sequence 29, Appl
7	39	66.1	140	4	US-09-270-767-48510	485.
٣	39	66.1	151	4	US-09-270-767-40030	
4	39	66.1	151	4		-
2	39	66.1	184	4	US-09-938-391A-13	
9	39	66.1	191	e	US-09-561-500-13	13,
7	39	66.1	191	n	US-09-561-108-13	13,
60	39	66.1	191	4	US-09-561-526-13	13,
Ø	39	66.1	191	4	US-09-561-499-13	13,
10	39	66.1	191	4	US-09-998-831-13	13,
11	39	66.1	191	4	US-09-561-005-13	13,
12	39	66.1	195	Н	US-08-159-784-2	2,
13	39	66.1	231	4	US-09-134-000C-5609	. 26(
14	38.5	65.3	818	4	US-09-462-845-3	
15	38.5	65.3	818	4	US-10-402-312-3	m
16	38	64.4	441	4	US-09-252-991A-32209	
17	37	62.7	346	4	US-09-540-236-3202	320
18	37	62.7	442	4	US-09-787-083-2	
19	37	62.7	442	4	US-09-787-083-4	4
20	37	62.7	442	4	US-09-787-083-6	Sequence 6, Appli
21	37	62.7	442	4	US-09-787-083-8	8
22	37	62.7	498	4	US-09-107-532A-5037	503
23	37	62.7	634	H	US-07-779-049-3	
24	37	62.7	634	Н	US-08-080-240-3	'n
25	36	61.0	189	4	US-09-270-767-38313	
26	36	61.0	189	4	US-09-270-767-53530	

Sequence 1677, Ap

4 US-09-702-705-1677

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1677, Ap	1677, Ap	1677, Ap	12683, A	14136, A	2, Appli	241, App	5575, Ap	5785, Ap	24504, A	23213, A	5244, Ap	3, Appli					
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
US-09-736-457-1677	US-09-671-325-1677	US-09-658-824-1677	US-09-902-540-12683	US-09-248-796A-14136	US-08-916-917-2	US-08-972-631-2	US-08-972-629-2	US-08-972-630-2	US-08-672-211-2	US-09-225-170-2	US-09-199-637A-241	US-09-621-976-5575	US-09-107-532A-5785	US-09-248-796A-24504	US-09-248-796A-23213	US-09-134-000C-5244	US-09-821-016-3
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36	36	36	36	36	36	36	36	36	36	36	35.5	35	35	35	35	35	35
28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

# ALIGNMENTS

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Sequence 29, Application US/09385442
| Patent No. 6200954
| GENERAL INFORMATION:
| APPLICANT: Ge, Ruowen
| APPLICANT: Kini, R. Manjunatha
| TITLE OF INVENTION: Small Peptides Having Potent Anti-Anglogenic Activity
| TITLE OF INVENTION NUMBER: US/09/385,442
| CURRENT APPLICATION NUMBER: 60/099,313
| CURRENT PILING DATE: 1999-09-04
| NUMBER OF SEQ ID NOS: 50
| SOFTWARE: PatentIn Ver. 2.0
| SEQ ID NO 29
| LENGTH: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 48510, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT PILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 48510
LENGTH: 140
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; ORGANISM: Drosophila melanogaster
US-09-270-767-48510
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Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
OTHER INFORMATION: Endo-1
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1 SPHNSYIVLPI 11
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US-09-270-767-48510
RESULT 1
US-09-385-442-29
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CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US PROV NO. 60/227,924
PRIOR FILING DATE: 2000-08-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin version 3.2
SEQ ID NO 13
LENGTH: 184
                                                                                                                                                                                                                                                                                                                                                                                       US-09-561-500-13
; Sequence 13, Application US/09561500
; Patent No. 6342219
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81.8%;
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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81.8%;
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Matches 9; Conservative
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Best Local Similarity 81.8
Matches 9; Conservative
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                                                                                                                                                 ORGANISM: MURINE US-09-938-391A-13
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US-09-561-108-13
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LENGTH: 191
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APPLICANT: Pfizer, Inc. and Pfizer Products, Inc.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING DISORDERS
TITLE OF INVENTION: INVOLVING ANGIOGENESIS
FILE REFERENCE: 3153.00234/PC10790A
CURRENT APPLICATION NUMBER: US/09/938,391A
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Sequence 55246, Application US/09270767

Patent No. 6703491

GENERAL INFORMATION:

TILLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILLE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270, 767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIN Ver. 2.0

LENGTH: 151
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i Sequence 40030, Application US/09270767

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i Generat No. 6703491

i TILE OF INVENTION:

i FILE REFERENCE: FILE Reference: 7326-094

i CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

i NUMBER OF SEQ ID NOS: 62517

i SOFTHARE: PatentIN Ver. 2.0

i SEQ ID NO 40030

i LENGTH: 151
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Pred. No. 13;
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Pred. No. 13;
3; Mismatches 1; Indela
     DB 4; Length 140;
12;
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                                            Mismatches
         Score 39;
Pred. No.
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US-09-398-391A-13
Sequence 13, Application US/09938391A
; Patent No. 6803211
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US-09-270-767-55246
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US-09-270-767-40030
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60.0%;
       Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 60.0%;
Matches 6; Conservative
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82 SPHNNHVNLP 91
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82 SPHNNHVNLP 91
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Best Local Similarity
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Sequence 13, Application US/09561108

Sequence 13, Application US/09561108

Sequence 13, Application US/09561108

Sequence 13, Application US/09561108

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE REFERENCE: 4001.002584

FILE REFERENCE: 4001.002584

CURRENT APPLICATION NUMBER: 60/131,432

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR APPLICATION NUMBER: 60/131,432

PRIOR PILING DATE: 1999-04-28

NUMBER OF SEQ ID NOS: 44

SOFTWARE: PATENTIN UVET: 2.0
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APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTIBODY COMPOSITIONS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002500
CURRENT FILING DATE: 2000-04-28
PRIOR PILING DATE: 1999-04-28
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEC ID NOS: 44
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 191
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Pred. No. 17;
ore 39; DB 4
ed. No. 16;
Mismatches
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  Score 39;
Pred. No.
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US-09-561-108-13

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US-09-561-005-13
                       US-09-998-831-13
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Sequence 13, Application US/09561526

Sequence 13, Application US/09561526

GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Breken
TITLE OF INVENTION: ANTIBODY CONJUGATE KITS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.00238
CURRENT FILING DATE: 2000-04-28
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 191
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APPLICANT: Philip E. Thorpe
APPLICANT: Philip E. Thorpe
APPLICANT: Polity E. Thorpe
TITLE CAMT: ROIf A. BERKEN
TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REPERENCE: 4001.002582
CURRENT PAPLICATION NUMBER: US/09/561,499
CURRENT FILING DATE: 1099-04-28
RICH APPLICATION NUMBER: 00/131,432
PRIOR FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN VOY: 2.0
SEQ ID NO 13
LENGTH: 191
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Score 39; DB 3; Length 191;
Pred. No. 17;
0; Mismatches 2; Indels
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Pred. No. 17;
0; Mismatches 2; Indels
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Patent No. 6524583
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ORGANISM: Artificial Sequence
    66.1%;
81.8%;
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Best Local Similarity 81.8%;
Matches 9; Conservative
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    Query Match 66.1
Best Local Similarity 81.8
Matches 9; Conservative
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Sequence 13. Application US/09561005
Sequence 13. Application US/09561005
GENERAL INFORMATION:
Patent NO. 6703020
GENERAL INFORMATION:
APPLICANT: Philip E. Thorpe
APPLICANT: Rolf A. Brekken
TITLE OF INVENTION: ANTHBODY CONJUGATE METHODS FOR SELECTIVELY INHIBITING VEGF
FILE REFERENCE: 4001.002585
CURRENT FAPLICATION NUMBER: US/09/561,005
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 191
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Sequence 13. Application US/09998831

Fateant No. 6676941

GENERAL INFORMATION:

APPLICANT: Philip E. Thorpe

APPLICANT: Rolf A. Brekken

TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY

TITLE OF INVENTION: INHIBITING VEGF

TITLE OF INVENTION: INHIBITING VEGF

TITLE OF INVENTION: ANTIBODY CONJUGATE COMPOSITIONS FOR SELECTIVELY

TITLE OF INVENTION: ANTIBODY CONJUGATE CONJUGAT
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; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-998-831-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC US-09-561-005-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Indels
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Pred. No. 17;
0; Mismatches
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US-08-159-784-2
; Sequence 2, Application US/08159784
; Patent No. 5643783
; GENERAL INFORMATION:
; APPLICANT: Bjorn R. Olsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66.1%;
81.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.0
Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           171 SCHNSYIVLCI 181
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Best Local Similarity
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181 APHGGFLVLPV 191

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TITLE OF INVENTION: NOVEL COLLAGEN AND USES THEREOF

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GENERAL INFORMATION:
APPLICANT: Estell, David A.
TITLE OF INVENTION: Proceases From Gram-Positive Organisms; TITLE OF INVENTION: Proceases From Gram-Positive Organisms; FILE REFERENCE: G232-US
CURRENT PILING DATE: 2000-01-13
PRIOR PELICATION NUMBER: PT/US98/14647
PRIOR APPLICATION NUMBER: EP 97305237.7
PRIOR FILING DATE: 1998-07-14
PRIOR PILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
US-10-402-312-3
; Sequence 3, Application US/10402312
; Patent No. 6833261
; GENERAL INFORMATION:
; APPLICANT: Estell, David A.
; TILLE OF INVENTION: Proteases From Gram-Positive Organisms FILE REFERENCE: GC382-US
; CURRENT APPLICATION NUMBER: US/10/402,312
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: PCT/US98/14647
; PRIOR PILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: E9 97305237.7
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3: BELLE OF THE OF
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Pred. No. 98;
2; Mismatches 1;
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                                                                                       ; Sequence 3, Application US/09462845; Patent No. 6723550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 65.3%;
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Best Local Similarity 63.0
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Best Local Similarity 63.6
Matches 7; Conservative
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                              RESULT 14
US-09-462-845-3
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Sequence 5609, Application US/09134000C

Sequence 5609, Application US/09134000C

Batent No. 6617156

GENERAL INFORMATION:

TITLE OF INVENTION: NUTCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: NUTRENCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR PILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

LENGTH: 231
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                                                                                                                                                COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,784
FILING DATE: December 1, 1993
CLASSIFICATION: 530
PRIOR APPLICATION: 530
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY, AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTOKNEILANDER: 29,066
RAMES JOHN FFERMER: 29,066
REFERENCE/DOCKET NUMBER: 0024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Enterococcus faecalis
US-09-134-000C-5609
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Best Local Similarity 81.8%;
Matches 9; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                Massachusetts
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STRANDEDNESS: N/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TOPOLOGY: N/A
US-08-159-784-2
                                                                                                 Boston
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TELEX: 20
                                                                STREET:
CITY: BO
STATE: M
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Indels

1 SPHNSYIVLPI 11

Length 818;